

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 5, 2005, 16:24:47 ; Search time 160 Seconds
(without alignments)

9.669 Million cell updates/sec

Title: US-09-697-590-2_COPY_292_295

Perfect score: 21

Sequence: 1 HARL 4

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	5	ABB81512 Neural th
2	21	100.0	4	6	ABJ19416 Neural th
3	21	100.0	5	5	ABB81511 Neural th
4	21	100.0	5	5	ABB81513 Neural th
5	21	100.0	5	6	ABJ19417 Neural th
6	21	100.0	5	6	ABJ19415 Neural th
7	21	100.0	6	5	ABB81528 Neural th
8	21	100.0	6	5	ABB81521 Neural th
9	21	100.0	6	5	ABB81514 Neural th
10	21	100.0	6	6	ABJ19442 Neural th
11	21	100.0	6	6	ABJ19432 Neural th
12	21	100.0	6	6	ABJ19418 Neural th
13	21	100.0	6	6	ABJ19425 Neural th
14	21	100.0	6	6	ABJ19443 Neural th
15	21	100.0	7	5	ABB81515 Neural th
16	21	100.0	7	5	ABB81517 Neural th
17	21	100.0	7	5	ABB81518 Neural th
18	21	100.0	7	6	ABJ19414 Neural th
19	21	100.0	7	6	ABJ19412 Neural th
20	21	100.0	7	6	ABJ19421 Neural th
21	21	100.0	7	6	ABJ19419 Neural th
22	21	100.0	7	6	ABJ19422 Neural th
23	21	100.0	7	6	ABJ19411 Neural th
24	21	100.0	8	5	ABB81537 Neural th
25	21	100.0	8	5	AAO22380 Protease

26	21	100.0	8	6	ABJ19441	Abj19441 Neural th
27	21	100.0	8	8	ADM73137	Adm73137 Human PRA
28	21	100.0	8	8	ADM73131	Adm73131 Human PRA
29	21	100.0	9	4	AAG99428	Aag99428 PRAME der
30	21	100.0	9	4	AAG99478	Aag99478 PRAME der
31	21	100.0	9	8	ADM73136	Adm73136 Human PRA
32	21	100.0	9	8	ADM73134	Adm73134 Human PRA
33	21	100.0	9	8	ADM73129	Adm73129 Human PRA
34	21	100.0	9	8	ADM73132	Adm73132 Human PRA
35	21	100.0	9	8	ADM73138	Adm73138 Human PRA
36	21	100.0	9	8	ADR23835	Adr23835 Human CNT
37	21	100.0	9	8	ADR23970	Adr23970 Human CNT
38	21	100.0	9	8	ADR23960	Adr23960 Human CNT
39	21	100.0	9	8	ADR23872	Adr23872 Human CNT
40	21	100.0	9	8	ADR23974	Adr23974 Human CNT
41	21	100.0	9	8	ADR23880	Adr23880 Human CNT
42	21	100.0	9	8	ADR23969	Adr23969 Human CNT
43	21	100.0	9	8	ADR23976	Adr23976 Human CNT
44	21	100.0	9	8	ADR23844	Adr23844 Human CNT
45	21	100.0	9	8	ADR23887	Adr23887 Human CNT
46	21	100.0	9	8	ADR23956	Adr23956 Human CNT
47	21	100.0	9	8	ADR23957	Adr23957 Human CNT
48	21	100.0	9	8	ADR23891	Adr23891 Human CNT
49	21	100.0	9	8	ADR23991	Adr23991 Human CNT
50	21	100.0	9	8	ADR23839	Adr23839 Human CNT
51	21	100.0	9	8	ADR23840	Adr23840 Human CNT
52	21	100.0	9	8	ADR23905	Adr23905 Human CNT
53	21	100.0	10	4	AAG99452	Aag99452 PRAME der
54	21	100.0	10	5	ABB81536	Abb81536 Neural th
55	21	100.0	10	6	ABJ19440	Abj19440 Neural th
56	21	100.0	10	8	ADM73128	Adm73128 Human PRA
57	21	100.0	10	8	ADM73135	Adm73135 Human PRA
58	21	100.0	10	8	ADM73130	Adm73130 Human PRA
59	21	100.0	10	8	ADM73133	Adm73133 Human PRA
60	21	100.0	11	8	ADP04309	Adp04309 Human thy
61	21	100.0	12	4	ABJ19437	Abj19437 Peptide 1
62	21	100.0	12	5	ABB81533	Abb81533 Neural th
63	21	100.0	12	6	ABJ19437	Abj19437 Neural th
64	21	100.0	13	5	ABB81532	Abb81532 Neural th
65	21	100.0	13	6	ABJ19436	Abj19436 Neural th
66	21	100.0	14	4	AAO00444	Aao00444 Human pro
67	21	100.0	14	4	AAO00412	Aao00412 Human pro
68	21	100.0	14	5	ABB81534	Abb81534 Neural th
69	21	100.0	14	6	ABU02988	Abu02988 Human neu
70	21	100.0	14	6	ABJ19438	Abj19438 Neural th
71	21	100.0	15	3	AAJ79924	Aaj79924 Human pap
72	21	100.0	15	5	ABB81535	Abb81535 Neural th
73	21	100.0	15	6	ABJ19439	Abj19439 Neural th
74	21	100.0	16	5	ABB81530	Abb81530 Neural th
75	21	100.0	16	6	ABU02984	Abu02984 Human neu
76	21	100.0	16	6	ABJ19434	Abj19434 Neural th
77	21	100.0	17	2	AAJ80293	Aaj80293 Trchalose
78	21	100.0	25	3	AAJ58899	Aaj58899 Polyketid
79	21	100.0	30	2	AAW94846	Aaw94846 Bait regi
80	21	100.0	30	3	AAJ56381	Aaj56381 Neisseria
81	21	100.0	30	5	AAU85095	Aau85095 Human PRA
82	21	100.0	31	2	AAU85096	Aau85096 Human PRA
83	21	100.0	31	2	AAW94447	Aaw94447 Mutant pr
84	21	100.0	31	8	ADM01215	Adm01215 Targeted
85	21	100.0	32	3	AAJ34676	Aaj34676 Human sec
86	21	100.0	32	4	AAJ17668	Aaj17668 Peptide #
87	21	100.0	32	4	ABB36687	Abb36687 Peptide #
88	21	100.0	32	4	AAJ30185	Aaj30185 Peptide #
89	21	100.0	32	4	ABB31475	Abb31475 Peptide #
90	21	100.0	32	4	ABB22024	Abb22024 Protein #
91	21	100.0	32	4	AAJ69846	Aaj69846 Human bon
92	21	100.0	32	4	AAJ57451	Aaj57451 Human bra
93	21	100.0	32	4	ABG51539	Abg51539 Human liv
94	21	100.0	32	4	AAO5331	Aao5331 Peptide #
95	21	100.0	32	5	ABG39474	Abg39474 Human pep
96	21	100.0	36	4	AAO09129	Aao09129 Human pol
97	21	100.0	37	4	AAO08247	Aao08247 Human pol
98	21	100.0	38	6	ABP80950	Abp80950 N. gonorr

XX 27-OCT-2000; 2000US-00697590.
 XX (NYMO-) NYMOX PHARM CORP.
 XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 XX WPI; 2002-507998/54.
 XX
 XX New Harlil peptide sequences of the Neural Thread Protein, useful in
 XX therapeutic assays, e.g. as targets for developing drugs for treating
 XX Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 XX these diseases.
 XX
 XX Claim 1; Page 29; 53pp; English.
 XX
 XX The present invention describes a neural thread protein (NTP) peptide
 XX having an amino acid sequence selected from ABB81511 to ABB81529 and
 XX their homologues, which are referred collectively as Harlil peptides (I).
 XX (I) have neuroprotective, nontropic, vasotropic and cerebroprotective
 XX activities, and can be used in peptide therapy. The Harlil peptide
 XX sequences can be used as analogues for NTP in therapeutic or diagnostic
 XX assays by replacing NTP with the peptide in such an assay. The Harlil
 XX peptides are also useful as a trap material in a diagnostic or
 XX therapeutic assay. Therefore, the Harlil peptides are useful in binding
 XX assays, protein and antibody purification, therapeutics or diagnostics.
 XX In particular, the peptides are also useful for diagnosing Alzheimer's
 XX disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 XX glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 XX are also useful as targets for drug development for the treatment of
 XX these diseases.
 XX Sequence 5 AA;
 XX
 XX Query Match 100.0%; Score 21; DB 5; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 HARL 4
 XX ||||
 XX Db 2 HARL 5
 XX
 XX RESULT 4
 XX ABB81513
 XX ID ABB81513 standard; peptide; 5 AA.
 XX
 XX AC ABB81513;
 XX
 XX DT 02-SEP-2002 (first entry)
 XX
 XX DE Neural thread protein (NTP) peptide #3.
 XX
 XX KW Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;
 XX Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 XX hypoxia; ischaemia; cerebral infarction.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200234915-A2.
 XX
 XX PD 02-MAY-2002.
 XX
 XX PF 25-OCT-2001; 2001WO-US042813.
 XX
 XX PR 27-OCT-2000; 2000US-00697590.
 XX
 XX PA (NYMO-) NYMOX PHARM CORP.
 XX
 XX PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 XX WPI; 2002-507998/54.
 XX

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 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
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 XX activities, and can be used in peptide therapy. The Harlil peptide
 XX sequences can be used as analogues for NTP in therapeutic or diagnostic
 XX assays by replacing NTP with the peptide in such an assay. The Harlil
 XX peptides are also useful as a trap material in a diagnostic or
 XX therapeutic assay. Therefore, the Harlil peptides are useful in binding
 XX assays, protein and antibody purification, therapeutics or diagnostics.
 XX In particular, the peptides are also useful for diagnosing Alzheimer's
 XX disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 XX glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 XX are also useful as targets for drug development for the treatment of
 XX these diseases.
 XX Sequence 5 AA;
 XX
 XX Query Match 100.0%; Score 21; DB 5; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 HARL 4
 XX ||||
 XX Db 1 HARL 4
 XX
 XX RESULT 5
 XX ABJ19417
 XX ID ABJ19417 standard; peptide; 5 AA.
 XX
 XX AC ABJ19417;
 XX
 XX DT 27-MAR-2003 (first entry)
 XX
 XX DE Neural thread protein peptide region #7.
 XX
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 XX neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX
 XX OS Unidentified.
 XX
 XX PN WO200292115-A2.
 XX
 XX PD 21-NOV-2002.
 XX
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX
 XX PA (NYMO-) NYMOX CORP.
 XX
 XX PI Averbach PA;
 XX
 XX DR WPI; 2003-129234/12.
 XX
 XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 XX tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 XX disease, by contacting the live tissue with at least one segment of
 XX neural thread proteins (NTP).
 XX
 XX PS Claim 2; Page 45; 60pp; English.
 XX
 XX The invention relates to a novel method for preventing and/or inhibiting
 XX cell death and/or tissue necrosis in a tissue comprising contacting the
 XX live tissue with at least one segment of neural thread proteins (NTP).

CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 1 HARL 4

RESULT 6

ABJ19415
 ID ABJ19415 standard; peptide; 5 AA.

XX AC ABJ19415;

XX DT 27-MAR-2003 (first entry)

XX DE Neural thread protein peptide region #5.

XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.

XX PN WO200292115-A2.

XX PD 21-NOV-2002.

XX PF 16-MAY-2002; 2002WO-CA000712.

XX PR 16-MAY-2001; 2001US-0290971P.

XX PA (NYMO-) NYMOX CORP.

XX PI Averbach PA;

XX DR WPT; 2003-129234/12.

XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).

XX PS Claim 2; Page 45; 60pp; English.

XX CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 2 HARL 5

RESULT 7

ABB81528
 ID ABB81528 standard; peptide; 6 AA.

XX

AC ABB81528;

XX DT 02-SEP-2002 (first entry)

XX DE Neural thread protein (NTP) peptide #18.

XX KW Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.

XX OS Homo sapiens.

XX PN WO200234915-A2.

XX PD 02-MAY-2002.

XX PF 25-OCT-2001; 2001WO-US042813.

XX PR 27-OCT-2000; 2000US-00697590.

XX PA (NYMO-) NYMOX PHARM CORP.

XX PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;

XX DR WPI; 2002-507998/54.

XX PT New Harilil peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases.

XX PS Claim 1; Page 29; 53pp; English.

XX CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Harilil peptides (I).
 CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harilil peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 21; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 1 HARL 4

RESULT 8

ABB81521
 ID ABB81521 standard; peptide; 6 AA.

XX AC ABB81521;

XX DT 02-SEP-2002 (first entry)

XX DE Neural thread protein (NTP) peptide #11.

XX KW Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.

PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).

PS Claim 2; Page 45; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting
XX cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 21; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 1 HARL 4

RESULT 11

ABJ19432
ID ABJ19432 standard; peptide; 6 AA.

XX AC ABJ19432;

XX 27-MAR-2003 (first entry)

XX Neural thread protein peptide region #22.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX Unidentified.

XX WO200292115-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-CA000712.

XX 16-MAY-2001; 2001US-0290971P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-129234/12.

XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).

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XX The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 21; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 1 HARL 4

RESULT 12

ABJ19418

ID ABJ19418 standard; peptide; 6 AA.

XX AC ABJ19418;

XX 27-MAR-2003 (first entry)

XX Neural thread protein peptide region #8.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX Unidentified.

XX WO200292115-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-CA000712.

XX 16-MAY-2001; 2001US-0290971P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-129234/12.

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PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
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CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 21; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 1 HARL 4

RESULT 13

ABJ19425

ID ABJ19425 standard; peptide; 6 AA.

XX AC ABJ19425;

XX 27-MAR-2003 (first entry)

XX Neural thread protein peptide region #15.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX Unidentified.

XX

PN WO200292115-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 16-MAY-2002; 2002WO-CA000712.
 XX
 PR 16-MAY-2001; 2001US-0290971P.
 XX
 PA (NYMO-) NYMOX CORP.
 XX
 XX Averbach PA;
 PI
 XX
 XX WPI; 2003-129234/12.
 DR
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
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 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 21; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db ||||
 1 HARL 4

RESULT 14
 ABJ19443
 ID ABJ19443 standard; peptide; 6 AA.
 XX
 AC ABJ19443;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 XX Neural thread protein peptide region #33.
 DE
 XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX
 XX Unidentified.
 OS
 XX WO200292115-A2.
 PN
 XX
 XX 21-NOV-2002.
 PD
 XX 16-MAY-2002; 2002WO-CA000712.
 PF
 XX 16-MAY-2001; 2001US-0290971P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach PA;
 PI
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 XX WPI; 2003-129234/12.
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 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
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 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 21; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db ||||
 1 HARL 4

RESULT 15
 ABB81515
 ID ABB81515 standard; peptide; 7 AA.
 XX
 AC ABB81515;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 XX Neural thread protein (NTP) peptide #5.
 DE
 XX Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 XX Homo sapiens.
 OS
 XX WO200234915-A2.
 PN
 XX 02-MAY-2002.
 PD
 XX 25-OCT-2001; 2001WO-US042813.
 PF
 XX 27-OCT-2000; 2000US-00697590.
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 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 21; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 2 HARL 5

RESULT 16

ABB81517
 ID ABB81517 standard; peptide; 7 AA.

AC ABB81517;
 XX

DT 02-SEP-2002 (first entry)
 XX

DE Neural thread protein (NTP) peptide #7.
 XX

XX Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX

OS Homo sapiens.
 XX

XX WO200234915-A2.
 PN

XX 02-MAY-2002.
 PD

XX 25-OCT-2001; 2001WO-US042813.
 PF

XX 27-OCT-2000; 2000US-00697590.
 PR

XX (NYMO-) NYMOX PHARM CORP.
 PA

XX Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 FI

XX WPI; 2002-507998/54.
 DR

XX New Harilil peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases.
 XX

PS Claim 1; Page 29; 53pp; English.
 XX

XX The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Harilil peptides (I).
 CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harilil peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 21; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 2 HARL 5

RESULT 17

ABB81518
 ID ABB81518 standard; peptide; 7 AA.

XX ABB81518;
 AC

XX 02-SEP-2002 (first entry)
 DT

XX Neural thread protein (NTP) peptide #8.
 DE

XX Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX

OS Homo sapiens.
 XX

XX WO200234915-A2.
 PN

XX 02-MAY-2002.
 PD

XX 25-OCT-2001; 2001WO-US042813.
 PF

XX 27-OCT-2000; 2000US-00697590.
 PR

XX (NYMO-) NYMOX PHARM CORP.
 PA

XX Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 FI

XX WPI; 2002-507998/54.
 DR

XX New Harilil peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases.
 XX

PS Claim 1; Page 29; 53pp; English.
 XX

XX The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Harilil peptides (I).
 CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harilil peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 21; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 2 HARL 5

RESULT 18

ABJ19414
 ID ABJ19414 standard; peptide; 7 AA.

XX ABJ19414;
 AC

XX 27-MAR-2003 (first entry)
 DT

XX DE Neural thread protein peptide region #4.
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.
 XX PN WO200292115-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA;
 XX XX
 XX XX WPI; 2003-129234/12.
 XX XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX XX
 XX PS Claim 2; Page 45; 60pp; English.
 XX CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX SQ Sequence 7 AA;
 XX
 XX Query Match 100.0%; Score 21; DB 6; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 2 HARL 5
 XX
 XX RESULT 19
 XX ABJ19412
 XX ID ABJ19412 standard; peptide; 7 AA.
 XX AC ABJ19412;
 XX DT 27-MAR-2003 (first entry)
 XX DE Neural thread protein peptide region #2.
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.
 XX PN WO200292115-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA;
 XX XX
 XX XX WPI; 2003-129234/12.
 XX XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX XX
 XX PS Claim 2; Page 45; 60pp; English.
 XX CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX SQ Sequence 7 AA;
 XX
 XX Query Match 100.0%; Score 21; DB 6; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 2 HARL 5
 XX
 XX RESULT 19
 XX ABJ19412
 XX ID ABJ19412 standard; peptide; 7 AA.
 XX AC ABJ19412;
 XX DT 27-MAR-2003 (first entry)
 XX DE Neural thread protein peptide region #2.
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.
 XX PN WO200292115-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA;
 XX XX

XX WPI; 2003-129234/12.
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX XX
 XX PS Claim 2; Page 45; 60pp; English.
 XX CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX SQ Sequence 7 AA;
 XX
 XX Query Match 100.0%; Score 21; DB 6; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 2 HARL 5
 XX
 XX RESULT 20
 XX ABJ19421
 XX ID ABJ19421 standard; peptide; 7 AA.
 XX AC ABJ19421;
 XX DT 27-MAR-2003 (first entry)
 XX DE Neural thread protein peptide region #11.
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.
 XX PN WO200292115-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA;
 XX XX
 XX XX WPI; 2003-129234/12.
 XX XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX XX
 XX PS Claim 2; Page 45; 60pp; English.
 XX CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX SQ Sequence 7 AA;
 XX

Query Match 100.0%; Score 21; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 21
ABJ19419
ID ABJ19419 standard; peptide; 7 AA.
XX
AC ABJ19419;
XX
DT 27-MAR-2003 (first entry)
XX
DE Neural thread protein peptide region #9.
XX
KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO200292115-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-CA000712.
XX
PR 16-MAY-2001; 2001US-0290971P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-129234/12.
XX
PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).
XX
PS Claim 2; Page 45; 60pp; English.
XX
CC The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 21; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 22
ABJ19422
ID ABJ19422 standard; peptide; 7 AA.
XX
AC ABJ19422;
XX
DT 27-MAR-2003 (first entry)
XX
DE Neural thread protein peptide region #12.
XX

Query Match 100.0%; Score 21; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 23
ABJ19411
ID ABJ19411 standard; peptide; 7 AA.
XX
AC ABJ19411;
XX
DT 27-MAR-2003 (first entry)
XX
DE Neural thread protein peptide region #1.
XX
KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO200292115-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-CA000712.
XX
PR 16-MAY-2001; 2001US-0290971P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-129234/12.
XX

PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).
XX
PS Claim 2; Page 45; 60pp; English.
XX
CC The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 21; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 HARL 4
Db 2 HARL 5
|||||
RESULT 24
ABB81537
ID ABB81537 standard; peptide; 8 AA.
XX
AC ABB81537;
XX
DT 02-SEP-2002 (first entry)
XX
DE Neural thread protein (NTP) peptide #27.
XX
XX Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
KW hypoxia; ischaemia; cerebral infarction.
XX
OS Homo sapiens.
XX
XX WO200234915-A2.
PN
XX
PD 02-MAY-2002.
XX
XX 25-OCT-2001; 2001WO-US042813.
PF
XX 27-OCT-2000; 2000US-00697590.
PR
XX (NYMO-) NYMOX PHARM CORP.
PA
XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
PI
XX WPI; 2002-507998/54.
DR
XX
XX New Harilil peptide sequences of the Neural Thread Protein, useful in
PT therapeutic assays, e.g. as targets for developing drugs for treating
PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
PT these diseases.
XX
PS Claim 3; Page 30; 53pp; English.
XX
CC The present invention describes a neural thread protein (NTP) peptide
CC having an amino acid sequence selected from ABB81511 to ABB81529 and
CC their homologues, which are referred collectively as Harilil peptides (I).
CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective
CC activities, and can be used in peptide therapy. The Harilil peptide
CC sequences can be used as analogues for NTP in therapeutic or diagnostic
CC assays by replacing NTP with the peptide in such an assay. The Harilil
CC peptides are also useful as a trap material in a diagnostic or
CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
CC assays, protein and antibody purification, therapeutics or diagnostics.
CC In particular, the peptides are also useful for diagnosing Alzheimer's

CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
CC are also useful as targets for drug development for the treatment of
CC these diseases. The present sequence represents a specifically claimed
CC peptide from the present invention
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 21; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 HARL 4
Db 3 HARL 6
|||||
RESULT 25
AAO22380
ID AAO22380 standard; peptide; 8 AA.
XX
AC AAO22380;
XX
DT 11-OCT-2002 (first entry)
XX
DE Protease cleavage site related peptide SEQ ID No 44.
XX
XX Cytostatic; antiinflammatory; antibacterial; matrix metalloproteinase;
KW protease cleavage site motif; enzyme; proteolytic enzyme; pathogenesis;
KW B. anthracis; pla; YopJ protease; versinia; smallpox HIL metalloprotease;
KW cathepsin family protease; TACE; calpain; caspase; BACE; beta-secretase;
KW tumour necrosis factor-alpha converting enzyme; blood clotting cascade;
KW beta-site amyloid precursor protein cleaving enzyme; presenilin; furin;
KW membrane-type serine protease; proprotein convertase; protease inhibitor;
KW proteasome; pathogenic infection; cancer; inflammatory disease.
XX
OS Homo sapiens.
XX
XX WO200238796-A2.
PN
XX
PD 16-MAY-2002.
XX
XX 08-NOV-2001; 2001WO-US046777.
PF
XX 08-NOV-2000; 2000US-0246815P.
PR
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA
XX Turk BE, Cantley LC;
PI
XX WPI; 2002-519316/55.
DR
XX
XX Rapid determination of protease cleavage site motifs using a mixture-
PT based oriented peptide library.
PT
XX
XX Example 1; Page 39; 126pp; English.
XX
CC The invention relates to a method for determining an amino acid sequence
CC motif for a cleavage site of a protease. The method comprises contacting
CC the protease with a peptide library containing degenerate residues which
CC allow for cleavage of a substrate by the protease, allowing the protease
CC to cleave peptides within the degenerate peptide library having a
CC cleavage site for the protease to form a population of cleaved peptides,
CC and determining an amino acid sequence motif for the cleavage site of the
CC protease. The protease of the method is a matrix metalloproteinase, or a
CC proteolytic enzyme that mediates the pathogenesis of a pathogen. The
CC protease is a lethal factor of B. anthracis, pla and YopJ proteases of
CC versinia, and the smallpox HIL metalloprotease. The protease of the
CC invention is selected from a protease of pathogenic organisms, cathepsin
CC family protease, tumour necrosis factor-alpha converting enzyme (TACE),
CC calpains, caspases, beta-site amyloid precursor protein cleaving enzyme
CC (BACE, beta-secretase), presenilins, membrane-type serine proteases,
CC furin and other proprotein convertases, proteasome components and

CC proteases affecting the blood clotting cascade. The protease inhibitors
CC of the invention are useful to treat diseases, including pathogenic
CC infections, cancer, and inflammatory diseases. This sequence represents a
CC peptide sequence relating to the protease cleavage site motifs of the
CC invention
XX
XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 2 HARL 5

RESULT 26

ABJ19441
ID ABJ19441 standard; peptide; 8 AA.

XX AC ABJ19441;

XX DT 27-MAR-2003 (first entry)

XX DE Neural thread protein peptide region #31.

XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
XX KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX OS Unidentified.

XX FN WO200292115-A2.

XX PD 21-NOV-2002.

XX PF 16-MAY-2002; 2002WO-CA000712.

XX PR 16-MAY-2001; 2001US-0290971P.

XX FA (NYMO-) NYMOX CORP.

XX PI Averbach PA;

XX DR WPI; 2003-129234/12.

XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
XX PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
XX PT disease, by contacting the live tissue with at least one segment of
XX PT neural thread proteins (NTP).

XX PS Claim 2; Page 45; 60pp; English.

XX CC The invention relates to a novel method for preventing and/or inhibiting
XX CC cell death and/or tissue necrosis in a tissue comprising contacting the
XX CC live tissue with at least one segment of neural thread proteins (NTP).
XX CC The methods are composition are useful for treating a neurodegenerative
XX CC disorder, such as Alzheimer's disease. This sequence represents an NTP
XX CC peptide of the invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 3 HARL 6

RESULT 27

ADM73137

ID ADM73137 standard; peptide; 8 AA.

XX AC ADM73137;

XX DT 03-JUN-2004 (first entry)

XX DE Human PRAME epitope SEQ ID NO:396.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX KW cancer; tumour; human; PRAME.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.

XX PA (MANN-) MANNKIND CORP.

XX PI Simard JYL, Diamond DC, Liu L, Liu Z;

XX DR WPI; 2004-315564/29.

XX PT New polypeptides and encoding nucleic acids that are useful epitopes of
XX PT target-associated antigens, useful for diagnosing and/or treating viral
XX PT infections, cancers and tumors.

XX PS Claim 1; SEQ ID NO 396; 357pp; English.

XX CC The present invention describes a polypeptide (I) comprising a component
XX CC selected from: (a) a polypeptide epitope having any of the 503 fully
XX CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
XX CC cluster comprising the polypeptide of (a); (c) a polypeptide having
XX CC substantial similarity to (a) or (b); (d) a polypeptide having functional
XX CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
XX CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
XX CC can be used in vaccines. The methods and compositions of the present
XX CC invention are useful for the diagnosis and/or treatment of viral
XX CC infections, cancers and tumors. The present sequence is used in the
XX CC exemplification of the present invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 1 HARL 4

RESULT 28

ADM73131

ID ADM73131 standard; peptide; 8 AA.

XX AC ADM73131;

XX DT 03-JUN-2004 (first entry)

XX DE Human PRAME epitope SEQ ID NO:390.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX KW cancer; tumour; human; PRAME.

XX OS Homo sapiens.

XX OS Synthetic.

PN WO2004022709-A2.
 XX 18-MAR-2004.
 XX
 PF 05-SEP-2003; 2003WO-US027706.
 XX
 PR 06-SEP-2002; 2002US-0409123P.
 XX
 PA (MANN-) MANNKIND CORP.
 XX
 PI Simard JUL, Diamond DC, Liu L, Liu Z;
 XX
 DR WPI; 2004-315564/29.
 XX
 XX
 PT New polypeptides and encoding nucleic acids that are useful epitopes of
 PT target-associated antigens, useful for diagnosing and/or treating viral
 PT infections, cancers and tumors.
 XX
 XX
 PS Claim 1; SEQ ID NO 390; 357pp; English.
 XX
 CC The present invention describes a polypeptide (I) comprising a component
 CC selected from: (a) a polypeptide epitope having any of the 503 fully
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
 CC can be used in vaccines. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of viral
 CC infections, cancers and tumors. The present sequence is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 21; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 5 HARL 8
 |||||
 RESULT 29
 ID AAG99428 standard; peptide; 9 AA.
 XX
 AC AAG99428;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 70.
 XX
 KW Vaccine; immune response; T cell response; epitope; proteasome; cancer;
 XX infection.
 XX Unidentified.
 XX
 PN EP1118860-A1.
 XX
 PD 25-JUL-2001.
 XX
 PF 21-JAN-2000; 2000EP-00200242.
 XX
 PR 21-JAN-2000; 2000EP-00200242.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;
 XX
 DR WPI; 2001-427158/46.
 XX
 XX

PT Selecting and/or producing a T cell epitope useful in a vaccine comprises
 PT subjecting a precursor peptide or polypeptide to the action of a 20S
 XX proteasome to determine the location of the C-terminus.
 XX
 PS Disclosure; Page 43; 102pp; English.
 XX
 CC The present invention describes a method of producing T cell epitopes,
 CC involving subjecting a precursor peptide to the action of a 20S
 CC proteasome, in order to locate the C-terminus of said epitope. This can
 CC be used in the production of vaccines, which can then be used to provoke
 CC a T cell response in the treatment of diseases such as cancer and
 CC infections. The present sequence is a peptide described in the
 CC exemplification of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 21; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 3 HARL 6
 |||||
 RESULT 30
 ID AAG99478 standard; peptide; 9 AA.
 XX
 AC AAG99478;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 120.
 XX
 KW Vaccine; immune response; T cell response; epitope; proteasome; cancer;
 XX infection.
 XX Unidentified.
 XX
 PN EP1118860-A1.
 XX
 PD 25-JUL-2001.
 XX
 PF 21-JAN-2000; 2000EP-00200242.
 XX
 PR 21-JAN-2000; 2000EP-00200242.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;
 XX
 DR WPI; 2001-427158/46.
 XX
 PT Selecting and/or producing a T cell epitope useful in a vaccine comprises
 PT subjecting a precursor peptide or polypeptide to the action of a 20S
 XX proteasome to determine the location of the C-terminus.
 XX
 PS Disclosure; Page 62; 102pp; English.
 XX
 CC The present invention describes a method of producing T cell epitopes,
 CC involving subjecting a precursor peptide to the action of a 20S
 CC proteasome, in order to locate the C-terminus of said epitope. This can
 CC be used in the production of vaccines, which can then be used to provoke
 CC a T cell response in the treatment of diseases such as cancer and
 CC infections. The present sequence is a peptide described in the
 CC exemplification of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 21; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 6 HARL 9

RESULT 31

ADM73136
ID ADM73136 standard; peptide; 9 AA.

XX AC ADM73136;

XX DT 03-JUN-2004 (first entry)

XX DE Human PRAME epitope SEQ ID NO:395.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX KW cancer; tumour; human; PRAME.

XX OS Homo sapiens.
XX OS Synthetic.

XX FN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.

XX PA (MANN-) MANNKIND CORP.

XX PI Simard JUL, Diamond DC, Liu L, Liu Z;

XX DR WPI; 2004-315564/29.

XX PT New polypeptides and encoding nucleic acids that are useful epitopes of
XX PT target-associated antigens, useful for diagnosing and/or treating viral
XX PT infections, cancers and tumors.

XX PS Claim 1; SEQ ID NO 395; 357pp; English.

XX CC The present invention describes a polypeptide (I) comprising a component
XX CC selected from: (a) a polypeptide epitope having any of the 503 fully
XX CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
XX CC cluster comprising the polypeptide of (a); (c) a polypeptide having
XX CC substantial similarity to (a) or (b); (d) a polypeptide having functional
XX CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
XX CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
XX CC can be used in vaccines. The methods and compositions of the present
XX CC invention are useful for the diagnosis and/or treatment of viral
XX CC infections, cancers and tumors. The present sequence is used in the
XX CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 2 HARL 5

RESULT 32

ADM73134
ID ADM73134 standard; peptide; 9 AA.

XX AC ADM73134;

XX DT 03-JUN-2004 (first entry)

XX DE Human PRAME epitope SEQ ID NO:393.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX KW cancer; tumour; human; PRAME.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.

XX XX (MANN-) MANNKIND CORP.

XX PI Simard JUL, Diamond DC, Liu L, Liu Z;

XX DR WPI; 2004-315564/29.

XX PT New polypeptides and encoding nucleic acids that are useful epitopes of
XX PT target-associated antigens, useful for diagnosing and/or treating viral
XX PT infections, cancers and tumors.

XX PS Claim 1; SEQ ID NO 393; 357pp; English.

XX CC The present invention describes a polypeptide (I) comprising a component
XX CC selected from: (a) a polypeptide epitope having any of the 503 fully
XX CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
XX CC cluster comprising the polypeptide of (a); (c) a polypeptide having
XX CC substantial similarity to (a) or (b); (d) a polypeptide having functional
XX CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
XX CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
XX CC can be used in vaccines. The methods and compositions of the present
XX CC invention are useful for the diagnosis and/or treatment of viral
XX CC infections, cancers and tumors. The present sequence is used in the
XX CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 3 HARL 6

RESULT 33

ADM73129
ID ADM73129 standard; peptide; 9 AA.

XX AC ADM73129;

XX DT 03-JUN-2004 (first entry)

XX DE Human PRAME epitope SEQ ID NO:388.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX KW cancer; tumour; human; PRAME.

XX OS Homo sapiens.
XX OS Synthetic.

XX FN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.
XX PA (MANN-) MANNKIND CORP.
XX PI Simard JYL, Diamond DC, Liu L, Liu Z;
XX DR WPI; 2004-315564/29.
XX PT New polypeptides and encoding nucleic acids that are useful epitopes of
XX PT target-associated antigens, useful for diagnosing and/or treating viral
XX PT infections, cancers and tumors.
XX PS Claim 1; SEQ ID NO 388; 357pp; English.
XX
CC The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db |||||
6 HARL 9
RESULT 34
ADM73132
ID ADM73132 standard; peptide; 9 AA.
AC ADM73132;
XX 03-JUN-2004 (first entry)
XX Human PRAME epitope SEQ ID NO:391.
XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX cancer; tumour; human; PRAME.
XX Homo sapiens.
XX Synthetic.
XX WO2004022709-A2.
XX 18-MAR-2004.
XX 05-SEP-2003; 2003WO-US027706.
XX 06-SEP-2002; 2002US-0409123P.
XX (MANN-) MANNKIND CORP.
XX Simard JYL, Diamond DC, Liu L, Liu Z;
XX WPI; 2004-315564/29.
XX New polypeptides and encoding nucleic acids that are useful epitopes of
XX target-associated antigens, useful for diagnosing and/or treating viral
XX infections, cancers and tumors.
XX Claim 1; SEQ ID NO 391; 357pp; English.
XX

XX CC The present invention describes a polypeptide (I) comprising a component
XX CC selected from: (a) a polypeptide epitope having any of the 503 fully
XX CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
XX CC cluster comprising the polypeptide of (a); (c) a polypeptide having
XX CC substantial similarity to (a) or (b); (d) a polypeptide having functional
XX CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
XX CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
XX CC can be used in vaccines. The methods and compositions of the present
XX CC invention are useful for the diagnosis and/or treatment of viral
XX CC infections, cancers and tumors. The present sequence is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db |||||
5 HARL 8
RESULT 35
ADM73138
ID ADM73138 standard; peptide; 9 AA.
XX ADM73138;
AC ADM73138;
XX 03-JUN-2004 (first entry)
XX Human PRAME epitope SEQ ID NO:397.
XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX cancer; tumour; human; PRAME.
XX Homo sapiens.
XX Synthetic.
XX WO2004022709-A2.
XX 18-MAR-2004.
XX 05-SEP-2003; 2003WO-US027706.
XX 06-SEP-2002; 2002US-0409123P.
XX (MANN-) MANNKIND CORP.
XX Simard JYL, Diamond DC, Liu L, Liu Z;
XX WPI; 2004-315564/29.
XX New polypeptides and encoding nucleic acids that are useful epitopes of
XX target-associated antigens, useful for diagnosing and/or treating viral
XX infections, cancers and tumors.
XX Claim 1; SEQ ID NO 397; 357pp; English.
XX
CC The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX SQ Sequence 9 AA;
XX

CC said variant protein. The computational protein design algorithm is used
 CC to assess the affinity of said variant protein for one or more receptor
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RTM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
 XX
 SQ

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db ||||
 5 HARL 8

RESULT 38
 ADR23960
 ID ADR23960 standard; peptide; 9 AA.
 XX
 AC ADR23960;
 XX
 DT 21-OCT-2004 (first entry)
 XX

DE Human CNTF class II MHC-binding less immunogenic variant #129.
 XX

KW immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.
 XX

OS Homo sapiens.
 XX

PN WO2004063963-A2.
 XX

PD 29-JUL-2004.
 XX

PF 08-JAN-2004; 2004WO-US000491.
 XX

PR 08-JAN-2003; 2003US-00339788.
 XX

PA (XENC-) XENCOR.
 XX

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
 XX

DR WPI; 2004-571511/55.
 XX

PT Generating, from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more
 PT variant sequences with an amino acid substitution in the parent protein.
 XX

PS Example 8; Page 64; 69pp; English.
 XX

CC The invention relates to a novel method for generating, from a parent
 CC protein, a variant protein having desired immunological and functional
 CC properties comprising generating one or more variant sequences comprising
 CC an amino acid substitution of a position of the first immunogenic
 CC sequence in the parent protein. The method comprises generating, from a
 CC parent protein, a variant protein having desired immunological and
 CC functional properties, the desired immunological property is enhanced
 CC uptake by antigen presenting cells (APCs). The desired immunological
 CC property is reduced or enhanced immunogenicity. The immunogenic sequence
 CC is selected from an antigen processing cleavage site, a class I MHC
 CC agretope, a class II MHC agretope, and an antibody epitope. The
 CC immunogenicity filter comprises a function that predicts antigen
 CC processing cleavage sites. The immunogenicity filter comprises a function
 CC that predicts class I or class II MHC agretopes. The immunogenicity

CC filter comprises a matrix method calculation. The immunogenicity filter
 CC comprises a function that predicts antibody epitopes. The computational
 CC protein design algorithm comprises a scoring function with two or more
 CC terms selected from the list: van der Waals, hydrogen bonding, the
 CC electrostatics, solvation, and secondary structure propensity. The
 CC computational protein design algorithm is used to assess the stability of
 CC said variant protein. The computational protein design algorithm is used
 CC to assess the affinity of said variant protein for one or more receptor
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RTM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
 XX
 SQ

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db ||||
 5 HARL 8

RESULT 39
 ADR23872
 ID ADR23872 standard; peptide; 9 AA.
 XX
 AC ADR23872;
 XX
 DT 21-OCT-2004 (first entry)
 XX

DE Human CNTF class II MHC-binding less immunogenic variant #41.
 XX

KW immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.
 XX

OS Homo sapiens.
 XX

PN WO2004063963-A2.
 XX

PD 29-JUL-2004.
 XX

PF 08-JAN-2004; 2004WO-US000491.
 XX

PR 08-JAN-2003; 2003US-00339788.
 XX

PA (XENC-) XENCOR.
 XX

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
 XX

DR WPI; 2004-571511/55.
 XX

PT Generating, from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more
 PT variant sequences with an amino acid substitution in the parent protein.
 XX
 PS Example 8; Page 62; 69pp; English.
 XX
 CC The invention relates to a novel method for generating, from a parent
 CC protein, a variant protein having desired immunological and functional
 CC properties comprising generating one or more variant sequences comprising
 CC an amino acid substitution of a position of the first immunogenic
 CC sequence in the parent protein. The method comprises generating, from a
 CC parent protein, a variant protein having desired immunological and
 CC functional properties, the desired immunological property is enhanced
 CC uptake by antigen presenting cells (APCs). The desired immunological

CC property is reduced or enhanced immunogenicity. The immunogenic sequence
 CC is selected from an antigen processing cleavage site, a class I MHC
 CC agretope, a class II MHC agretope, and an antibody epitope. The
 CC immunogenicity filter comprises a function that predicts antigen
 CC processing cleavage sites. The immunogenicity filter comprises a function
 CC that predicts class I or class II MHC agretopes. The immunogenicity
 CC filter comprises a matrix method calculation. The immunogenicity filter
 CC comprises a function that predicts antibody epitopes. The computational
 CC protein design algorithm comprises a scoring function with two or more
 CC terms selected from the list: van der Waals, hydrogen bonding,
 CC electrostatics, solvation, and secondary structure propensity. The
 CC computational protein design algorithm is used to assess the stability of
 CC said variant protein. The computational protein design algorithm is used
 CC to assess the affinity of said variant protein for one or more receptor
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RTM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 5 HARL 8

RESULT 40
 ADR23974
 ID ADR23974 standard; peptide; 9 AA.
 AC ADR23974;
 XX
 XX 21-OCT-2004 (first entry)
 DT Human CNTF class II MHC-binding less immunogenic variant #143.
 DE immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.
 XX
 OS Homo sapiens.
 XX
 XX WO2004063963-A2.
 XX
 XX 29-JUL-2004.
 PD
 XX
 PF 08-JAN-2004; 2004WO-US000491.
 XX
 XX 08-JAN-2003; 2003US-00339788.
 PR (XENC-) XENCOR.
 XX
 XX Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
 PI WPI; 2004-571511/55.
 DR
 XX
 XX Generating from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more
 PT variant sequences with an amino acid substitution in the parent protein.
 XX
 XX Example 9; Page 65; 69pp; English.
 PS
 XX
 XX The invention relates to a novel method for generating, from a parent
 CC protein, a variant protein having desired immunological and functional

CC properties comprising generating one or more variant sequences comprising
 CC an amino acid substitution of a position of the first immunogenic
 CC sequence in the parent protein. The method comprises generating, from a
 CC parent protein, a variant protein having desired immunological and
 CC functional properties, the desired immunological property is enhanced
 CC uptake by antigen presenting cells (APCs). The desired immunological
 CC property is reduced or enhanced immunogenicity. The immunogenic sequence
 CC is selected from an antigen processing cleavage site, a class I MHC
 CC agretope, a class II MHC agretope, and an antibody epitope. The
 CC immunogenicity filter comprises a function that predicts antigen
 CC processing cleavage sites. The immunogenicity filter comprises a function
 CC that predicts class I or class II MHC agretopes. The immunogenicity
 CC filter comprises a matrix method calculation. The immunogenicity filter
 CC comprises a function that predicts antibody epitopes. The computational
 CC protein design algorithm comprises a scoring function with two or more
 CC terms selected from the list: van der Waals, hydrogen bonding,
 CC electrostatics, solvation, and secondary structure propensity. The
 CC computational protein design algorithm is used to assess the stability of
 CC said variant protein. The computational protein design algorithm is PDA
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RTM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 5 HARL 8

RESULT 41
 ADR23880
 ID ADR23880 standard; peptide; 9 AA.
 AC ADR23880;
 XX
 XX 21-OCT-2004 (first entry)
 DT Human CNTF class II MHC-binding less immunogenic variant #49.
 DE immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.
 XX
 OS Homo sapiens.
 XX
 XX WO2004063963-A2.
 XX
 XX 29-JUL-2004.
 PD
 XX
 PF 08-JAN-2004; 2004WO-US000491.
 XX
 XX 08-JAN-2003; 2003US-00339788.
 PR (XENC-) XENCOR.
 XX
 XX Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
 PI WPI; 2004-571511/55.
 DR
 XX
 XX Generating from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more

variant sequences with an amino acid substitution in the parent protein.
Example 8; Page 62; 69pp; English.

The invention relates to a novel method for generating, from a parent protein, a variant protein having desired immunological and functional properties comprising generating one or more variant sequences comprising an amino acid substitution of a position of the first immunogenic sequence in the parent protein. The method comprises generating, from a parent protein, a variant protein having desired immunological and functional properties, the desired immunological property is enhanced uptake by antigen presenting cells (APCs). The desired immunological property is reduced or enhanced immunogenicity. The immunogenic sequence is selected from an antigen processing cleavage site, a class I MHC agretope, a class II MHC agretope, and an antibody epitope. The immunogenicity filter comprises a function that predicts antigen processing cleavage sites. The immunogenicity filter comprises a function that predicts class I or class II MHC agretopes. The immunogenicity filter comprises a matrix method calculation. The immunogenicity filter comprises a function that predicts antibody epitopes. The computational protein design algorithm comprises a scoring function with two or more terms selected from the list: van der Waals, hydrogen bonding, electrostatics, solvation, and secondary structure propensity. The computational protein design algorithm is used to assess the stability of said variant protein. The computational protein design algorithm is used to assess the affinity of said variant protein for one or more receptor or ligand molecules. The computational protein design algorithm is PDA (RTM) technology. The method further comprises experimentally generating the variant protein, recovering the variant protein, and administering the variant protein to a patient. The method is useful for generating a variant protein with altered immunogenicity, preferably for identifying modifications that increase or decrease the immunogenicity of a protein by affecting antigen uptake. The present sequence represents a class II MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 42

ADR23969
ID ADR23969 standard; peptide; 9 AA.

AC ADR23969;

DT 21-OCT-2004 (first entry)

DE Human CNTF class II MHC-binding less immunogenic variant #138.

immunogenic; antigen presenting cell; APC;
antigen processing cleavage site; class I MHC agretope;
class II MHC agretope; antibody epitope; CNTF;
ciliary neurotrophic factor.

Homo sapiens.

WO2004063963-A2.

29-JUL-2004.

08-JAN-2004; 2004WO-US000491.

08-JAN-2003; 2003US-00339788.

(XENC-) XENCOR.

XX

PT

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PT

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Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

WPI; 2004-571511/55.

Generating, from a parent protein, a variant protein having desired immunological and functional properties, comprises generating one or more variant sequences with an amino acid substitution in the parent protein.

Example 9; Page 65; 69pp; English.

The invention relates to a novel method for generating, from a parent protein, a variant protein having desired immunological and functional properties comprising generating one or more variant sequences comprising an amino acid substitution of a position of the first immunogenic sequence in the parent protein. The method comprises generating, from a parent protein, a variant protein having desired immunological and functional properties, the desired immunological property is enhanced uptake by antigen presenting cells (APCs). The desired immunological property is reduced or enhanced immunogenicity. The immunogenic sequence is selected from an antigen processing cleavage site, a class I MHC agretope, a class II MHC agretope, and an antibody epitope. The immunogenicity filter comprises a function that predicts antigen processing cleavage sites. The immunogenicity filter comprises a function that predicts class I or class II MHC agretopes. The immunogenicity filter comprises a matrix method calculation. The immunogenicity filter comprises a function that predicts antibody epitopes. The computational protein design algorithm comprises a scoring function with two or more terms selected from the list: van der Waals, hydrogen bonding, electrostatics, solvation, and secondary structure propensity. The computational protein design algorithm is used to assess the stability of said variant protein. The computational protein design algorithm is used to assess the affinity of said variant protein for one or more receptor or ligand molecules. The computational protein design algorithm is PDA (RTM) technology. The method further comprises experimentally generating the variant protein, recovering the variant protein, and administering the variant protein to a patient. The method is useful for generating a variant protein with altered immunogenicity, preferably for identifying modifications that increase or decrease the immunogenicity of a protein by affecting antigen uptake. The present sequence represents a class II MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 43

ADR23976
ID ADR23976 standard; peptide; 9 AA.

AC ADR23976;

DT 21-OCT-2004 (first entry)

DE Human CNTF class II MHC-binding less immunogenic variant #145.

immunogenic; antigen presenting cell; APC;

antigen processing cleavage site; class I MHC agretope;

class II MHC agretope; antibody epitope; CNTF;

ciliary neurotrophic factor.

Homo sapiens.

WO2004063963-A2.

29-JUL-2004.

XX

XX

XX

XX

XX

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PF 08-JAN-2004; 2004WO-US000491.
XX
PR 08-JAN-2003; 2003US-00339788.
XX
XX (XENC-) XENCOR.
XX
PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
XX
XX WPI; 2004-571511/55.
XX
PT Generating, from a parent protein, a variant protein having desired
PT immunological and functional properties, comprises generating one or more
PT variant sequences with an amino acid substitution in the parent protein.
XX
XX Example 9; Page 66; 69pp; English.
XX
CC The invention relates to a novel method for generating, from a parent
CC protein, a variant protein having desired immunological and functional
CC properties comprising generating one or more variant sequences comprising
CC an amino acid substitution of a position of the first immunogenic
CC sequence in the parent protein. The method comprises generating, from a
CC parent protein, a variant protein having desired immunological and
CC functional properties, the desired immunological property is enhanced
CC uptake by antigen presenting cells (APCs). The desired immunological
CC property is reduced or enhanced immunogenicity. The immunogenic sequence
CC is selected from an antigen processing cleavage site, a class I MHC
CC agretope, a class II MHC agretope, and an antibody epitope. The
CC immunogenicity filter comprises a function that predicts antigen
CC processing cleavage sites. The immunogenicity filter comprises a function
CC that predicts class I or class II MHC agretopes. The immunogenicity
CC filter comprises a matrix method calculation. The immunogenicity filter
CC comprises a function that predicts antibody epitopes. The computational
CC protein design algorithm comprises a scoring function with two or more
CC terms selected from the list: van der Waals, hydrogen bonding,
CC electrostatics, solvation, and secondary structure propensity. The
CC computational protein design algorithm is used to assess the stability of
CC said variant protein. The computational protein design algorithm is used
CC or ligand molecules. The computational protein design algorithm is PDA
CC (RTM) technology. The method further comprises experimentally generating
CC the variant protein, recovering the variant protein, and administering
CC the variant protein to a patient. The method is useful for generating a
CC variant protein with altered immunogenicity, preferably for identifying
CC modifications that increase or decrease the immunogenicity of a protein
CC by affecting antigen uptake. The present sequence represents a class II
CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HARL 4
Db 5 HARL 8
|||
|||
RESULT 44
ID ADR23844 standard; peptide; 9 AA.
XX
AC ADR23844;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human CNTF class II MHC-binding less immunogenic variant #13.
XX
KW immunogenic; antigen presenting cell; APC;
KW antigen processing cleavage site; class I MHC agretope;
KW class II MHC agretope; antibody epitope; CNTF;
KW ciliary neurotrophic factor.
XX

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OS Homo sapiens.
XX
PN WO2004063963-A2.
XX
XX 29-JUL-2004.
XX
PF 08-JAN-2004; 2004WO-US000491.
XX
XX 08-JAN-2003; 2003US-00339788.
XX
XX (XENC-) XENCOR.
XX
PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
XX
XX WPI; 2004-571511/55.
XX
XX Generating, from a parent protein, a variant protein having desired
XX immunological and functional properties, comprises generating one or more
XX variant sequences with an amino acid substitution in the parent protein.
XX
XX Example 8; Page 61; 69pp; English.
XX
CC The invention relates to a novel method for generating, from a parent
CC protein, a variant protein having desired immunological and functional
CC properties comprising generating one or more variant sequences comprising
CC an amino acid substitution of a position of the first immunogenic
CC sequence in the parent protein. The method comprises generating, from a
CC parent protein, a variant protein having desired immunological and
CC functional properties, the desired immunological property is enhanced
CC uptake by antigen presenting cells (APCs). The desired immunological
CC property is reduced or enhanced immunogenicity. The immunogenic sequence
CC is selected from an antigen processing cleavage site, a class I MHC
CC agretope, a class II MHC agretope, and an antibody epitope. The
CC immunogenicity filter comprises a function that predicts antigen
CC processing cleavage sites. The immunogenicity filter comprises a function
CC that predicts class I or class II MHC agretopes. The immunogenicity
CC filter comprises a matrix method calculation. The immunogenicity filter
CC comprises a function that predicts antibody epitopes. The computational
CC protein design algorithm comprises a scoring function with two or more
CC terms selected from the list: van der Waals, hydrogen bonding,
CC electrostatics, solvation, and secondary structure propensity. The
CC computational protein design algorithm is used to assess the stability of
CC said variant protein. The computational protein design algorithm is PDA
CC or ligand molecules. The computational protein design algorithm is PDA
CC (RTM) technology. The method further comprises experimentally generating
CC the variant protein, recovering the variant protein, and administering
CC the variant protein to a patient. The method is useful for generating a
CC variant protein with altered immunogenicity, preferably for identifying
CC modifications that increase or decrease the immunogenicity of a protein
CC by affecting antigen uptake. The present sequence represents a class II
CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
XX
XX Sequence 9 AA;
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HARL 4
Db 5 HARL 8
|||
|||
RESULT 45
AD23887
ID ADR23887 standard; peptide; 9 AA.
XX
AC ADR23887;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human CNTF class II MHC-binding less immunogenic variant #56.

```


XX immunogenic; antigen presenting cell; APC;
KW antigen processing cleavage site; class I MHC agretope;
KW class II MHC agretope; antibody epitope; CNTF;
KW ciliary neurotrophic factor.
XX Homo sapiens.
OS
XX WO2004063963-A2.
XX 29-JUL-2004.
XX
PF 08-JAN-2004; 2004WO-US000491.
XX
PR 08-JAN-2003; 2003US-00339788.
XX
PA (XENC-) XENCOR.
XX
PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
XX WPI; 2004-571511/55.
XX
PS Generating, from a parent protein, a variant protein having desired
XX immunological and functional properties, comprises generating one or more
PT variant sequences with an amino acid substitution in the parent protein.
XX
XX Example 8; Page 62; 69pp; English.
XX
CC The invention relates to a novel method for generating, from a parent
CC protein, a variant protein having desired immunological and functional
CC properties comprising generating one or more variant sequences comprising
CC an amino acid substitution of a position of the first immunogenic
CC sequence in the parent protein. The method comprises generating, from a
CC parent protein, a variant protein having desired immunological and
CC functional properties, the desired immunological property is enhanced
CC uptake by antigen presenting cells (APCs). The desired immunological
CC property is reduced or enhanced immunogenicity. The immunogenic sequence
CC is selected from an antigen processing cleavage site, a class I MHC
CC agretope, a class II MHC agretope, and an antibody epitope. The
CC immunogenicity filter comprises a function that predicts antigen
CC processing cleavage sites. The immunogenicity filter comprises a function
CC that predicts class I or class II MHC agretopes. The immunogenicity
CC filter comprises a matrix method calculation. The immunogenicity filter
CC comprises a function that predicts antibody epitopes. The computational
CC protein design algorithm comprises a scoring function with two or more
CC terms selected from the list: van der Waals, hydrogen bonding,
CC electrostatics, solvation, and secondary structure propensity. The
CC computational protein design algorithm is used to assess the stability of
CC said variant protein. The computational protein design algorithm is used
CC to assess the affinity of said variant protein for one or more receptor
CC or ligand molecules. The computational protein design algorithm is PDA
CC (RTM) technology. The method further comprises experimentally generating
CC the variant protein, recovering the variant protein, and administering
CC the variant protein to a patient. The method is useful for generating a
CC variant protein with altered immunogenicity, preferably for identifying
CC modifications that increase or decrease the immunogenicity of a protein
CC by affecting antigen uptake. The present sequence represents a class II
CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
| | | |
Db 5 HARL 8
| | | |
RESULT 46
ADR23956
ID ADR23956 standard; peptide; 9 AA.

XX ADR23956;
AC 21-OCT-2004 (first entry)
DT
XX Human CNTF class II MHC-binding less immunogenic variant #125.
DE
XX immunogenic; antigen presenting cell; APC;
KW antigen processing cleavage site; class I MHC agretope;
KW class II MHC agretope; antibody epitope; CNTF;
KW ciliary neurotrophic factor.
XX
XX Homo sapiens.
OS
XX WO2004063963-A2.
XX 29-JUL-2004.
XX
PF 08-JAN-2004; 2004WO-US000491.
XX
PR 08-JAN-2003; 2003US-00339788.
XX
PA (XENC-) XENCOR.
XX
PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;
XX WPI; 2004-571511/55.
XX
PS Generating, from a parent protein, a variant protein having desired
XX immunological and functional properties, comprises generating one or more
PT variant sequences with an amino acid substitution in the parent protein.
XX
XX Example 8; Page 64; 69pp; English.
XX
CC The invention relates to a novel method for generating, from a parent
CC protein, a variant protein having desired immunological and functional
CC properties comprising generating one or more variant sequences comprising
CC an amino acid substitution of a position of the first immunogenic
CC sequence in the parent protein. The method comprises generating, from a
CC parent protein, a variant protein having desired immunological and
CC functional properties, the desired immunological property is enhanced
CC uptake by antigen presenting cells (APCs). The desired immunological
CC property is reduced or enhanced immunogenicity. The immunogenic sequence
CC is selected from an antigen processing cleavage site, a class I MHC
CC agretope, a class II MHC agretope, and an antibody epitope. The
CC immunogenicity filter comprises a function that predicts antigen
CC processing cleavage sites. The immunogenicity filter comprises a function
CC that predicts class I or class II MHC agretopes. The immunogenicity
CC filter comprises a matrix method calculation. The immunogenicity filter
CC comprises a function that predicts antibody epitopes. The computational
CC protein design algorithm comprises a scoring function with two or more
CC terms selected from the list: van der Waals, hydrogen bonding,
CC electrostatics, solvation, and secondary structure propensity. The
CC computational protein design algorithm is used to assess the stability of
CC said variant protein. The computational protein design algorithm is used
CC to assess the affinity of said variant protein for one or more receptor
CC or ligand molecules. The computational protein design algorithm is PDA
CC (RTM) technology. The method further comprises experimentally generating
CC the variant protein, recovering the variant protein, and administering
CC the variant protein to a patient. The method is useful for generating a
CC variant protein with altered immunogenicity, preferably for identifying
CC modifications that increase or decrease the immunogenicity of a protein
CC by affecting antigen uptake. The present sequence represents a class II
CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
| | | |

Db 5 HARL 8

RESULT 47

ADR23957

ID ADR23957 standard; peptide; 9 AA.

XX

AC ADR23957;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human CNTF class II MHC-binding less immunogenic variant #126.

XX

XX immunogenic; antigen presenting cell; APC;

KW antigen processing cleavage site; class I MHC agretope;

KW class II MHC agretope; antibody epitope; CNTF;

KW ciliary neurotrophic factor.

XX

OS Homo sapiens.

XX

XX WO2004063963-A2.

FN

XX 29-JUL-2004.

PD

XX

PF 08-JAN-2004; 2004WO-US000491.

XX

XX 08-JAN-2003; 2003US-00339788.

PR

XX (XENC-) XENCOR.

PA

XX Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

PI

XX WPI; 2004-571511/55.

DR

XX

PT Generating, from a parent protein, a variant protein having desired immunological and functional properties, comprises generating one or more variant sequences with an amino acid substitution in the parent protein.

PT

XX

PS Example 8; Page 64; 69pp; English.

XX

CC The invention relates to a novel method for generating, from a parent protein, a variant protein having desired immunological and functional properties comprising generating one or more variant sequences comprising an amino acid substitution of a position of the first immunogenic sequence in the parent protein. The method comprises generating, from a parent protein, a variant protein having desired immunological and functional properties, the desired immunological property is enhanced uptake by antigen presenting cells (APCs). The desired immunological property is reduced or enhanced immunogenicity. The immunogenic sequence is selected from an antigen processing cleavage site, a class I MHC agretope, a class II MHC agretope, and an antibody epitope. The immunogenicity filter comprises a function that predicts antigen processing cleavage sites. The immunogenicity filter comprises a matrix method calculation. The immunogenicity filter comprises a function that predicts antibody epitopes. The computational protein design algorithm comprises a scoring function with two or more terms selected from the list: van der Waals, hydrogen bonding, electrostatics, solvation, and secondary structure propensity. The computational protein design algorithm is used to assess the stability of or ligand molecules. The computational protein design algorithm is PDA (RTM) technology. The method further comprises experimentally generating the variant protein, recovering the variant protein, and administering a variant protein with altered immunogenicity, preferably for identifying modifications that increase or decrease the immunogenicity of a protein by affecting antigen uptake. The present sequence represents a class II MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX

Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;

Best Local Similarity 100.0%; Pred No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

DB 5 HARL 8

RESULT 48

ADR23891

ID ADR23891 standard; peptide; 9 AA.

XX

AC ADR23891;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human CNTF class II MHC-binding less immunogenic variant #60.

XX

XX immunogenic; antigen presenting cell; APC;

KW antigen processing cleavage site; class I MHC agretope;

KW class II MHC agretope; antibody epitope; CNTF;

KW ciliary neurotrophic factor.

XX

OS Homo sapiens.

XX

XX WO2004063963-A2.

FN

XX 29-JUL-2004.

PD

XX

PF 08-JAN-2004; 2004WO-US000491.

XX

XX 08-JAN-2003; 2003US-00339788.

PR

XX (XENC-) XENCOR.

PA

XX Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

PI

XX WPI; 2004-571511/55.

DR

XX

PT Generating, from a parent protein, a variant protein having desired immunological and functional properties, comprises generating one or more variant sequences with an amino acid substitution in the parent protein.

PT

XX

PS Example 8; Page 63; 69pp; English.

XX

CC The invention relates to a novel method for generating, from a parent protein, a variant protein having desired immunological and functional properties comprising generating one or more variant sequences comprising an amino acid substitution of a position of the first immunogenic sequence in the parent protein. The method comprises generating, from a parent protein, a variant protein having desired immunological and functional properties, the desired immunological property is enhanced uptake by antigen presenting cells (APCs). The desired immunological property is reduced or enhanced immunogenicity. The immunogenic sequence is selected from an antigen processing cleavage site, a class I MHC agretope, a class II MHC agretope, and an antibody epitope. The immunogenicity filter comprises a function that predicts antigen processing cleavage sites. The immunogenicity filter comprises a matrix method calculation. The immunogenicity filter comprises a function that predicts antibody epitopes. The computational protein design algorithm comprises a scoring function with two or more terms selected from the list: van der Waals, hydrogen bonding, electrostatics, solvation, and secondary structure propensity. The computational protein design algorithm is used to assess the stability of or ligand molecules. The computational protein design algorithm is PDA (RTM) technology. The method further comprises experimentally generating the variant protein, recovering the variant protein, and administering a variant protein with altered immunogenicity, preferably for identifying modifications that increase or decrease the immunogenicity of a protein by affecting antigen uptake. The present sequence represents a class II MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX

Sequence 9 AA;

CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 5 HARL 8

RESULT 49

ADR23991

ID ADR23991 standard; peptide; 9 AA.

AC ADR23991;

DT 21-OCT-2004 (first entry)

DE Human CNTF class II MHC-binding less immunogenic variant #160.

KW immunogenic; antigen presenting cell; APC;

KW antigen processing cleavage site; class I MHC agretope;

KW class II MHC agretope; antibody epitope; CNTF;

KW ciliary neurotrophic factor.

OS Homo sapiens.

PN WO2004063963-A2.

PD 29-JUL-2004.

PF 08-JAN-2004; 2004WO-US000491.

PR 08-JAN-2003; 2003US-00339788.

PA (XENC-) XENCOR.

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

DR WPI; 2004-571511/55.

PS Generating, from a parent protein, a variant protein having desired

PT immunological and functional properties, comprises generating one or more

PT variant sequences with an amino acid substitution in the parent protein.

PS Example 9; Page 66; 69pp; English.

CC The invention relates to a novel method for generating, from a parent

CC protein, a variant protein having desired immunological and functional

CC properties comprising generating one or more variant sequences comprising

CC an amino acid substitution of a position of the first immunogenic

CC sequence in the parent protein. The method comprises generating, from a

CC parent protein, a variant protein having desired immunological and

CC to assess the affinity of said variant protein for one or more receptor

CC (RTM) molecules. The computational protein design algorithm is PDA

CC the variant protein, recovering the variant protein, and administering a

CC variant protein to a patient. The method is useful for generating a

CC variant protein with altered immunogenicity, preferably for identifying

CC modifications that increase or decrease the immunogenicity of a protein

CC by affecting antigen uptake. The present sequence represents a class II

CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 5 HARL 8

RESULT 50

ADR23839

ID ADR23839 standard; peptide; 9 AA.

AC ADR23839;

DT 21-OCT-2004 (first entry)

DE Human CNTF class II MHC-binding less immunogenic variant #8.

KW immunogenic; antigen presenting cell; APC;

KW antigen processing cleavage site; class I MHC agretope;

KW class II MHC agretope; antibody epitope; CNTF;

KW ciliary neurotrophic factor.

OS Homo sapiens.

PN WO2004063963-A2.

PD 29-JUL-2004.

PF 08-JAN-2004; 2004WO-US000491.

PR 08-JAN-2003; 2003US-00339788.

PA (XENC-) XENCOR.

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

DR WPI; 2004-571511/55.

PS Generating, from a parent protein, a variant protein having desired

PT immunological and functional properties, comprises generating one or more

PT variant sequences with an amino acid substitution in the parent protein.

XX Example 8; Page 61; 69pp; English.

CC The invention relates to a novel method for generating, from a parent

CC protein, a variant protein having desired immunological and functional

CC properties comprising generating one or more variant sequences comprising

CC an amino acid substitution of a position of the first immunogenic

CC sequence in the parent protein. The method comprises generating, from a

CC parent protein, a variant protein having desired immunological and

CC functional properties, the desired immunological property is enhanced

CC uptake by antigen presenting cells (APCs). The desired immunological

CC property is reduced or enhanced immunogenicity. The immunogenic sequence

CC is selected from an antigen processing cleavage site, a class I MHC

CC agretope, a class II MHC agretope, and an antibody epitope. The

CC immunogenicity filter comprises a function that predicts antigen

CC processing cleavage sites. The immunogenicity filter comprises a function

CC that predicts class I or class II MHC agretopes. The immunogenicity

CC filter comprises a matrix method calculation. The immunogenicity

CC filter comprises a function that predicts antibody epitopes. The computational

CC protein design algorithm comprises a scoring function with two or more

CC terms selected from the list: van der Waals, hydrogen bonding,

CC electrostatics, solvation, and secondary structure propensity. The

CC computational protein design algorithm is used to assess the stability of

CC said variant protein. The computational protein design algorithm is used

CC comprises a function that predicts antibody epitopes. The computational
 CC protein design algorithm comprises a scoring function with two or more
 CC terms selected from the list: van der Waals, hydrogen bonding,
 CC electrostatics, solvation, and secondary structure propensity. The
 CC computational protein design algorithm is used to assess the stability of
 CC said variant protein. The computational protein design algorithm is used
 CC to assess the affinity of said variant protein for one or more receptor
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RPM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 5 HARL 8
 ||||

RESULT 51
 ADR23840
 ID ADR23840 standard; peptide; 9 AA.

XX ADR23840;

XX 21-OCT-2004 (first entry)

XX Human CNTF class II MHC-binding less immunogenic variant #9.

XX immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.

XX Homo sapiens.

XX WO2004063963-A2.

XX 29-JUL-2004.

XX 08-JAN-2004; 2004WO-US000491.

XX 08-JAN-2003; 2003US-00339788.

XX (XENC-) XENCOR.

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

XX WPI; 2004-571511/55.

XX Generating, from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more
 PT variant sequences with an amino acid substitution in the parent protein.

XX Example 8; Page 61; 69pp; English.

XX The invention relates to a novel method for generating, from a parent
 CC protein, a variant protein having desired immunological and functional
 CC properties comprising generating one or more variant sequences comprising
 CC an amino acid substitution of a position of the first immunogenic
 CC sequence in the parent protein. The method comprises generating, from a
 CC parent protein, a variant protein having desired immunological and
 CC functional properties, the desired immunological property is enhanced
 CC uptake by antigen presenting cells (APCs). The desired immunological
 CC property is reduced or enhanced immunogenicity. The immunogenic sequence

CC is selected from an antigen processing cleavage site, a class I MHC
 CC agretope, a class II MHC agretope, and an antibody epitope. The
 CC immunogenicity filter comprises a function that predicts antigen
 CC processing cleavage sites. The immunogenicity filter comprises a function
 CC that predicts class I or class II MHC agretopes. The immunogenicity
 CC filter comprises a matrix method calculation. The immunogenicity filter
 CC comprises a function that predicts antibody epitopes. The computational
 CC protein design algorithm comprises a scoring function with two or more
 CC terms selected from the list: van der Waals, hydrogen bonding, the
 CC electrostatics, solvation, and secondary structure propensity. The
 CC computational protein design algorithm is used to assess the stability of
 CC said variant protein. The computational protein design algorithm is used
 CC to assess the affinity of said variant protein for one or more receptor
 CC or ligand molecules. The computational protein design algorithm is PDA
 CC (RPM) technology. The method further comprises experimentally generating
 CC the variant protein, recovering the variant protein, and administering
 CC the variant protein to a patient. The method is useful for generating a
 CC variant protein with altered immunogenicity, preferably for identifying
 CC modifications that increase or decrease the immunogenicity of a protein
 CC by affecting antigen uptake. The present sequence represents a class II
 CC MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 5 HARL 8
 ||||

RESULT 52
 ADR23905

ID ADR23905 standard; peptide; 9 AA.

XX ADR23905;

XX 21-OCT-2004 (first entry)

XX Human CNTF class II MHC-binding less immunogenic variant #74.

XX immunogenic; antigen presenting cell; APC;
 KW antigen processing cleavage site; class I MHC agretope;
 KW class II MHC agretope; antibody epitope; CNTF;
 KW ciliary neurotrophic factor.

XX Homo sapiens.

XX WO2004063963-A2.

XX 29-JUL-2004.

XX 08-JAN-2004; 2004WO-US000491.

XX 08-JAN-2003; 2003US-00339788.

XX (XENC-) XENCOR.

PI Chirino AJ, Dahiyat BI, Desjarlais JR, Marshall SA;

XX WPI; 2004-571511/55.

XX Generating, from a parent protein, a variant protein having desired
 PT immunological and functional properties, comprises generating one or more
 PT variant sequences with an amino acid substitution in the parent protein.

XX Example 8; Page 63; 69pp; English.

XX The invention relates to a novel method for generating, from a parent
 CC protein, a variant protein having desired immunological and functional
 CC properties comprising generating one or more variant sequences comprising

an amino acid substitution of a position of the first immunogenic sequence in the parent protein. The method comprises generating, from a parent protein, a variant protein having desired immunological and functional properties, the desired immunological property is enhanced uptake by antigen presenting cells (APCs). The desired immunological property is reduced or enhanced immunogenicity. The immunological sequence is selected from an antigen processing cleavage site, a class I MHC agretope, a class II MHC agretope, and an antibody epitope. The immunogenicity filter comprises a function that predicts antigen processing cleavage sites. The immunogenicity filter comprises a function that predicts class I or class II MHC agretopes. The immunogenicity filter comprises a matrix method calculation. The immunogenicity filter comprises a function that predicts antibody epitopes. The computational protein design algorithm comprises a scoring function with two or more terms selected from the list: van der Waals, hydrogen bonding, electrostatics, solvation, and secondary structure propensity. The computational protein design algorithm is used to assess the stability of said variant protein. The computational protein design algorithm is used to assess the affinity of said variant protein for one or more receptor or ligand molecules. The computational protein design algorithm is PDA (RTM) technology. The method further comprises experimentally generating the variant protein, recovering the variant protein, and administering the variant protein to a patient. The method is useful for generating a variant protein with altered immunogenicity, preferably for identifying modifications that increase or decrease the immunogenicity of a protein by affecting antigen uptake. The present sequence represents a class II MHC-binding peptide from human ciliary neurotrophic factor (CNTF).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 53

AAG99452
ID AAG99452 standard; peptide; 10 AA.

AC AAG99452;

DT 01-OCT-2001 (first entry)

XX PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 94.

DE Vaccine; immune response; T cell response; epitope; proteasome; cancer; infection.

XX Unidentified.

XX EP1118860-A1.

XX 25-JUL-2001.

XX 21-JAN-2000; 2000EP-00200242.

XX 21-JAN-2000; 2000EP-00200242.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX Ossendorp F, Offringa R, Melief CJM, Kessler JH;

XX WPI; 2001-427158/46.

XX Selecting and/or producing a T cell epitope useful in a vaccine comprises PT subjecting a precursor peptide or polypeptide to the action of a 20S PT proteasome to determine the location of the C-terminus.

PS Disclosure; Page 52; 102pp; English.
XX The present invention describes a method of producing T cell epitopes, CC involving subjecting a precursor peptide to the action of a 20S CC proteasome, in order to locate the C-terminus of said epitope. This can CC be used in the production of vaccines, which can then be used to provoke CC a T cell response in the treatment of diseases such as cancer and CC infections. The present sequence is a peptide described in the CC exemplification of the invention

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 21; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 54

ABB81536
ID ABB81536 standard; peptide; 10 AA.

AC ABB81536;

DT 02-SEP-2002 (first entry)

XX Neural thread protein (NTP) peptide #26.

XX Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;

XX Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma; hypoxia; ischaemia; cerebral infarction.

XX Homo sapiens.

XX WO200234915-A2.

XX 02-MAY-2002.

XX 25-OCT-2001; 2001WO-US042813.

XX 27-OCT-2000; 2000US-00697590.

XX (NYMO-) NYMOX PHARM CORP.

XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;

XX WPI; 2002-507998/54.

XX New Harlil peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing PT these diseases.

XX Claim 3; Page 30; 53pp; English.

XX The present invention describes a neural thread protein (NTP) peptide CC having an amino acid sequence selected from ABB81511 to ABB81529 and CC their homologues, which are referred collectively as Harlil peptides (I). CC (I) have neuroprotective, neurotropic, vasotropic and cerebroprotective CC activities, and can be used in peptide therapy. The Harlil peptide CC sequences can be used as analogues for NTP in therapeutic or diagnostic CC assays by replacing NTP with the peptide in such an assay. The Harlil CC peptides are also useful as a trap material in a diagnostic or CC therapeutic assay. Therefore, the Harlil peptides are useful in binding CC assays, protein and antibody purification, therapeutics or diagnostics. CC In particular, the peptides are also useful for diagnosing Alzheimer's CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas, CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides CC are also useful as targets for drug development for the treatment of CC these diseases. The present sequence represents a specifically claimed

```
CC peptide from the present invention
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 21; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 55
ABJ19440
ID ABJ19440 standard; peptide; 10 AA.
XX
AC ABJ19440;
XX
DT 27-MAR-2003 (first entry)
XX
XX Neural thread protein peptide region #30.
DE
XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
XX neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX
XX Unidentified.
XX
XX WO200292115-A2.
XX
XX 21-NOV-2002.
XX
XX 16-MAY-2002; 2002WO-CA000712.
XX
XX 16-MAY-2001; 2001US-0290971P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-129234/12.
XX
XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
XX tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
XX disease, by contacting the live tissue with at least one segment of
XX neural thread proteins (NTP).
XX
XX Claim 2; Page 45; 60pp; English.
XX
XX The invention relates to a novel method for preventing and/or inhibiting
XX cell death and/or tissue necrosis in a tissue comprising contacting the
XX live tissue with at least one segment of neural thread proteins (NTP).
XX The methods are composition are useful for treating a neurodegenerative
XX disorder, such as Alzheimer's disease. This sequence represents an NTP
XX peptide of the invention
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 21; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 56
ADM73128
ID ADM73128 standard; peptide; 10 AA.
XX
AC ADM73128;
XX

03-JUN-2004 (first entry)
XX
Human PRAME epitope SEQ ID NO:387.
XX
epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX cancer; tumour; human; PRAME.
XX
Homo sapiens.
XX Synthetic.
XX
WO2004022709-A2.
XX
18-MAR-2004.
XX
05-SEP-2003; 2003WO-US027706.
XX
06-SEP-2002; 2002US-0409123P.
XX
(MANN-) MANNKIND CORP.
XX
Simard J.L., Diamond DC, Liu L, Liu Z;
XX
WPI; 2004-315564/29.
XX
New polypeptides and encoding nucleic acids that are useful epitopes of
XX target-associated antigens, useful for diagnosing and/or treating viral
XX infections, cancers and tumors.
XX
Claim 1; SEQ ID NO 387; 357pp; English.
XX
The present invention describes a polypeptide (I) comprising a component
XX selected from: (a) a polypeptide epitope having any of the 503 fully
XX defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
XX cluster comprising the polypeptide of (a); (c) a polypeptide having
XX substantial similarity to (a) or (b); (d) a polypeptide having functional
XX similarity to any of (a)-(c); or (e) a nucleic acid encoding the
XX polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
XX can be used in vaccines. The methods and compositions of the present
XX invention are useful for the diagnosis and/or treatment of viral
XX infections, cancers and tumours. The present sequence is used in the
XX exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 21; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 7 HARL 10

RESULT 57
ADM73135
ID ADM73135 standard; peptide; 10 AA.
XX
AC ADM73135;
XX
03-JUN-2004 (first entry)
XX
Human PRAME epitope SEQ ID NO:394.
XX
epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
XX cancer; tumour; human; PRAME.
XX
Homo sapiens.
XX Synthetic.
XX
WO2004022709-A2.
XX
18-MAR-2004.
XX
```

PF 05-SEP-2003; 2003WO-US027706.
XX
PR 06-SEP-2002; 2002US-0409123P.
XX
PA (MANN-) MANNKIND CORP.
XX
PI Simard JUL, Diamond DC, Liu L, Liu Z;
XX
DR WPI; 2004-315564/29.
XX
XX New polypeptides and encoding nucleic acids that are useful epitopes of
PT target-associated antigens, useful for diagnosing and/or treating viral
PT infections, cancers and tumors.
XX
PS Claim 1; SEQ ID NO 394; 357pp; English.
XX
CC The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 21; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db 3 HARL 6
RESULT 58
ADM73130
ID ADM73130 standard; peptide; 10 AA.
AC
XX ADM73130;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PRAME epitope SEQ ID NO:389.
XX
KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
KW cancer; tumour; human; PRAME.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004022709-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027706.
XX
PR 06-SEP-2002; 2002US-0409123P.
XX
PA (MANN-) MANNKIND CORP.
XX
PI Simard JUL, Diamond DC, Liu L, Liu Z;
XX
DR WPI; 2004-315564/29.
XX
XX New polypeptides and encoding nucleic acids that are useful epitopes of
PT target-associated antigens, useful for diagnosing and/or treating viral
PT infections, cancers and tumors.
XX

PS Claim 1; SEQ ID NO 389; 357pp; English.
XX
CC The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 21; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db 6 HARL 9
RESULT 59
ADM73133
ID ADM73133 standard; peptide; 10 AA.
AC ADM73133;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PRAME epitope SEQ ID NO:392.
XX
KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
KW cancer; tumour; human; PRAME.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004022709-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027706.
XX
PR 06-SEP-2002; 2002US-0409123P.
XX
PA (MANN-) MANNKIND CORP.
XX
PI Simard JUL, Diamond DC, Liu L, Liu Z;
XX
DR WPI; 2004-315564/29.
XX
XX New polypeptides and encoding nucleic acids that are useful epitopes of
PT target-associated antigens, useful for diagnosing and/or treating viral
PT infections, cancers and tumors.
XX
PS Claim 1; SEQ ID NO 392; 357pp; English.
XX
CC The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX

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SQ Sequence 10 AA;
Query Match 100.0%; Score 21; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 4 HARL 7

RESULT 60
ADP04309
ID ADP04309 standard; peptide; 11 AA.
XX
AC ADP04309;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human thyroperoxidase, TPO, peptide residues 353-363, SEQ ID 1.
XX
KW Cytostatic; Immunosuppressive; Thyromimetic; Antithyroid; human;
KW thyroperoxidase; hTPO; immunodominant region; MPO homology domain;
KW myeloperoxidase homology domain; CCP homology domain;
KW complement-control protein homology domain; autoimmune disease;
KW thyroid disease; Graves' disease; Hashimoto disease; thyroid cancer.
XX
OS Homo sapiens.
XX
FN FR2848566-A1.
XX
PD 18-JUN-2004.
XX
PF 11-DEC-2002; 2002FR-00015657.
XX
PR 11-DEC-2002; 2002FR-00015657.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Peraldi RS, Bes C, Bresson D, Charles T, Devauchelle G;
PI Cerutti M;
XX
DR WPI; 2004-452913/43.
XX
PT New peptides recognized by autoantibodies against human thyroperoxidase,
PT useful for diagnosis and treatment of autoimmune diseases and thyroid
PT cancer, also antibodies specific for them.
XX
PS Claim 3; SEQ ID NO 1; 64pp; French.
XX
CC The present invention relates to novel peptides (I; ADP04313-ADP04324)
CC which are recognized by autoantibodies (AAB) directed against human
CC thyroperoxidase (hTPO). (I) comprise a discontinuous epitope derived from
CC the discontinuous immunodominant region of hTPO, consisting of four
CC distinct regions that are homologous to MPO (myeloperoxidase) or CCP
CC (complement-control protein). (I) contain at least one of the cryptic
CC motifs given in ADP04325-ADP04327. The discontinuous epitope comprises
CC hTPO regions 353-363 (ADP04309); 377-386 (ADP04310) and 713-720
CC (ADP04311) of the MPO homology domain and 766-775 (ADP04312) of the CCP
CC homology domain. (I) are used to detect AAB, particularly for diagnosis
CC of autoimmune diseases (especially of the thyroid, e.g. Graves' and
CC Hashimoto diseases) or thyroid cancers. Also (I), and anti-TPO antibodies
CC that recognize them, are useful for treating these diseases. To
CC illustrate the invention, TPO mutants were made. The present sequence is
CC the wild-type peptide sequence which was replaced with the ADP04328
CC peptide.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 21; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 4 HARL 7

RESULT 61
AAB31270
ID AAB31270 standard; peptide; 12 AA.
XX
AC AAB31270;
XX
DT 20-APR-2001 (first entry)
XX
DE Peptide ligand which binds to human MUC1 protein.
XX
KW MUC1; epithelial cell mucin; tumour; MUC1 ligand; cancer.
XX
OS Synthetic.
XX
FN WO200077031-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-CA000711.
XX
PR 15-JUN-1999; 99US-0139263P.
XX
PA (UYHE-) UNIV HEALTH NETWORK.
XX
PI Gariepy J, Yang S;
XX
FN WPI; 2001-091388/10.
XX
PT Novel ligands that binds to MUC1, an epithelial cell mucin, useful for
PT diagnosing, monitoring, treating and preventing cancer.
XX
PS Claim 15; Page 42; 60pp; English.
XX
CC The present sequence represents a peptide ligand which binds to human
CC MUC1 protein. MUC1 is an epithelial cell mucin, which is found on, and
CC shed from, the surface of many tumours. MUC1 peptide ligands were
CC isolated using a phage display technique using MUC1 tandem repeats as the
CC target. The MUC1 tandem target repeats comprise repeats of the peptide
CC AAB31258. The ligands are useful for detecting the presence of MUC1 in a
CC sample, to treat or prevent cancer associated with MUC1 and to prepare a
CC medicament or diagnostic agent to treat, prevent or detect cancer
CC associated with MUC1. By assaying for the binding between the MUC1 ligand
CC and MUC1 in a sample diagnosis or monitoring of cancer can be carried
CC out. The ligands may also be used to prepare antibodies
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 21; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 7 HARL 10

RESULT 62
ABB81533
ID ABB81533 standard; peptide; 12 AA.
XX
AC ABB81533;
XX
DT 02-SEP-2002 (first entry)
XX
DE Neural thread protein (NTP) peptide #23.
XX
KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;

```


KW hypoxia; ischaemia; cerebral infarction.

XX Homo sapiens.

OS WO200234915-A2.

PN 02-MAY-2002.

FD 25-OCT-2001; 2001WO-US042813.

XX 27-OCT-2000; 2000US-00697590.

XX (NYMO-) NYMOX PHARM CORP.

XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;

XX WPI; 2002-507998/54.

XX New Harllil peptide sequences of the Neural Thread Protein, useful in
PT therapeutic assays, e.g. as targets for developing drugs for treating
PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
PT these diseases.

XX Claim 3; Page 30; 53pp; English.

XX The present invention describes a neural thread protein (NTP) peptide
CC having an amino acid sequence selected from ABB81511 to ABB81529 and
CC their homologues, which are referred collectively as Harllil peptides (I).
CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective
CC activities, and can be used in peptide therapy. The Harllil peptide
CC sequences can be used as analogues for NTP in therapeutic or diagnostic
CC assays by replacing NTP with the peptide in such an assay. The Harllil
CC peptides are also useful as a trap material in a diagnostic or
CC therapeutic assay. Therefore, the Harllil peptides are useful in binding
CC assays, protein and antibody purification, therapeutics or diagnostics.
CC In particular, the peptides are also useful for diagnosing Alzheimer's
CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
CC are also useful as targets for drug development for the treatment of
CC these diseases. The present sequence represents a specifically claimed
CC peptide from the present invention

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 21; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 2 HARL 5

RESULT 63

ABJ19437

ID ABJ19437 standard; peptide; 12 AA.

XX AC ABJ19437;

XX DT 27-MAR-2003 (first entry)

XX Neural thread protein peptide region #27.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;

XX neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX Unidentified.

XX WO200292115-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-CA000712.

XX

PR 16-MAY-2001; 2001US-0290971P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-129234/12.

XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).

XX Claim 2; Page 45; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC peptide of the invention

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 21; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 2 HARL 5

RESULT 64

ABB81532

ID ABB81532 standard; peptide; 13 AA.

XX AC ABB81532;

XX DT 02-SEP-2002 (first entry)

XX Neural thread protein (NTP) peptide #22.

XX Neural thread protein; NTP; Harllil peptide; Alzheimer's disease;

XX Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;

XX hypoxia; ischaemia; cerebral infarction.

XX Homo sapiens.

XX WO200234915-A2.

XX 02-MAY-2002.

XX 25-OCT-2001; 2001WO-US042813.

XX 27-OCT-2000; 2000US-00697590.

XX (NYMO-) NYMOX PHARM CORP.

XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;

XX WPI; 2002-507998/54.

XX New Harllil peptide sequences of the Neural Thread Protein, useful in
PT therapeutic assays, e.g. as targets for developing drugs for treating
PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
PT these diseases.

XX Claim 3; Page 29; 53pp; English.

XX The present invention describes a neural thread protein (NTP) peptide
CC having an amino acid sequence selected from ABB81511 to ABB81529 and

CC their homologues, which are referred collectively as Harlil peptides (I).

CC (I) have neuroprotective, neurotropic, vasotropic and cerebroprotective

CC activities, and can be used in peptide therapy. The Harlil peptide

CC sequences can be used as analogues for NTP in therapeutic or diagnostic

CC assays by replacing NTP with the peptide in such an assay. The Harlil

CC peptides are also useful as a trap material in a diagnostic or

CC therapeutic assay. Therefore, the Harlil peptides are useful in binding

CC assays, protein and antibody purification, therapeutics or diagnostics.

CC In particular, the peptides are also useful for diagnosing Alzheimer's

CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,

CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides

CC are also useful as targets for drug development for the treatment of

CC these diseases. The present sequence represents a specifically claimed

CC peptide from the present invention

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 21; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
| | | |

Db 9 HARL 12

RESULT 65

ABJ19436

ID ABJ19436 standard; peptide; 13 AA.

XX

AC ABJ19436;

XX

DT 27-MAR-2003 (first entry)

XX

DE Neural thread protein peptide region #25.

XX

KW Neurotropic; neuroprotective; cell death; tissue necrosis; NTP;

KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX

OS Unidentified.

XX

PN WO200292115-A2.

XX

PD 21-NOV-2002.

XX

PF 16-MAY-2002; 2002WO-CA000712.

XX

PR 16-MAY-2001; 2001US-0290971P.

XX

PA (NYMO-) NYMOX CORP.

XX

FI Averbach PA;

XX

DR WPI; 2003-129234/12.

XX

PT Preventing and/or inhibiting cell death and/or tissue necrosis in a

PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's

PT disease, by contacting the live tissue with at least one segment of

PT neural thread proteins (NTP).

XX

PS Claim 2; Page 45; 60pp; English.

XX

CC The invention relates to a novel method for preventing and/or inhibiting

CC cell death and/or tissue necrosis in a tissue comprising contacting the

CC live tissue with at least one segment of neural thread proteins (NTP).

CC The methods are composition are useful for treating a neurodegenerative

CC disorder, such as Alzheimer's disease. This sequence represents an NTP

CC peptide of the invention

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 21; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
| | | |

Db 5 HARL 8

RESULT 67

AAM00412

ID AAM00412 standard; peptide; 14 AA.

XX

AC AAM00412;

XX

DT 01-OCT-2001 (first entry)

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
| | | |

Db 9 HARL 12

RESULT 66

AAM00444

ID AAM00444 standard; peptide; 14 AA.

XX

AC AAM00444;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human protein fragment SEQ ID NO: 992.

XX

KW Human; single nucleotide polymorphism; SNP; paternity test;

KW forensic test; aberrant protein expression.

XX

OS Homo sapiens.

XX

PN WO200151670-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JAN-2001; 2001WO-US000322.

XX

PR 07-JAN-2000; 2000US-0174962P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX

DR WPI; 2001-451871/48.

XX

DR N-PSDB; AAH89561.

XX

PT Isolated human polynucleotides containing single nucleotide

PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,

PT infection and diabetes.

XX

PS Disclosure; Page 388; 475pp; English.

XX

CC The present invention relates to human nucleic acids containing single

CC nucleotide polymorphisms (SNPs). These can be used in forensic and

CC paternity tests, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, diabetes,

CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,

CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,

CC meningitis, muscular disorders, dementia, neurological diseases, tubercu-

CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,

CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or

CC autoimmunity. The present sequence is a peptide encoded by a

CC polymorphism-containing oligonucleotide fragment of the invention

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 21; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
| | | |

Db 5 HARL 8

XX DE Human protein fragment SEQ ID NO: 960.
 XX KW Human; single nucleotide polymorphism; SNP; paternity test;
 KW KW forensic test; aberrant protein expression.
 XX OS Homo sapiens.
 XX PN WO200151670-A2.
 XX PD 19-JUL-2001.
 XX PF 05-JAN-2001; 2001WO-US000322.
 XX PR 07-JAN-2000; 2000US-0174962P.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach MD;
 XX WPI; 2001-451871/48.
 DR N-PSDB; AAH89529.
 XX Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes.
 XX Disclosure; Page 379; 475pp; English.
 XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention
 XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 21; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 5 HARL 8

RESULT 68
 ABB81534
 ID ABB81534 standard; peptide; 14 AA.
 XX ABB81534;
 AC ABB81534;
 XX 02-SEP-2002 (first entry)
 DT
 DE Neural thread protein (NTP) peptide #24.
 XX Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX Homo sapiens.
 OS
 XX WO200234915-A2.
 PN
 XX 02-MAY-2002.
 PD
 XX 25-OCT-2001; 2001WO-US042813.
 PF

XX PR 27-OCT-2000; 2000US-00697590.
 XX PA (NYMO-) NYMOX PHARM CORP.
 XX PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 XX WPI; 2002-507998/54.
 DR
 XX New Harlil peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases.
 XX Claim 3; Page 30; 53pp; English.
 XX The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Harlil peptides (1).
 CC (1) have neuroprotective, nootropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harlil peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harlil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harlil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases. The present sequence represents a specifically claimed
 CC peptide from the present invention
 XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 5 HARL 8

RESULT 69
 ABU02988
 ID ABU02988 standard; peptide; 14 AA.
 XX ABU02988;
 AC
 XX 20-JAN-2003 (first entry)
 DT
 XX Human neural thread protein AD7C-NTP, peptide fragment #8.
 DE
 XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
 KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
 KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
 KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
 KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
 KW cosmetic modification; vascular disease; atherosclerosis;
 KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
 KW autoimmune disease; metabolic disease; traumatic disease;
 KW physical injury; nutritional deficiency disease; infectious disease;
 KW amyloid disease; fibrosis disease; storage disease; poisoning;
 KW congenital malformation; enzyme deficiency disease; radiation;
 KW intoxication; environmental disease; radiation disease;
 KW endocrine disease; degenerative disease; mechanical disease.
 XX Homo sapiens.
 OS
 XX WO200297030-A2.
 PN
 XX 05-DEC-2002.
 PD

XX PS Disclosure; Fig 10; 110pp; English.
 CC The present invention describes the use of a small organic compound (A)
 CC which competitively inhibits interaction of a papillomavirus (PV) E2
 CC protein with a PV E1 protein for treating a cell infected with PV or a
 CC mammal with a PV-induced condition. (A) has antiviral, virucide,
 CC cytostatic, antiproliferative and dermatological activities. Methods from
 CC the present invention can be used to treat PV-induced conditions
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
 CC lesions chosen from warts and other benign cutaneous lesions, planar
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's common
 CC warts, flat warts, genital warts (condyloma acuminatum) and
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal, oesophageal
 CC and other upper airway papilloma or vaginal, cervical, vulvar, penile and
 CC anorectal carcinoma. The E2 inhibitors may also be used to treat
 CC epithelial and internal fibropapillomas in animals. The present sequence
 CC represents a peptide sequence used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 3 HARL 6

RESULT 72
 ABB81535
 ID ABB81535 standard; peptide; 15 AA.
 XX
 AC ABB81535;
 DT 02-SEP-2002 (first entry)
 XX
 DE Neural thread protein (NTP) peptide #25.
 XX
 KW Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 25-OCT-2001; 2001WO-US042813.
 XX
 PR 27-OCT-2000; 2000US-00697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.
 XX

PT New Harilil peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases.
 XX
 PS Claim 3; Page 30; 53pp; English.
 XX

CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Harilil peptides (I).
 CC (I) have neuroprotective, neurotropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harilil peptide

CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases. The present sequence represents a specifically claimed
 CC peptide from the present invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 11 HARL 14

RESULT 73
 ABJ19439
 ID ABJ19439 standard; peptide; 15 AA.

XX
 AC ABJ19439;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE Neural thread protein peptide region #29.

XX
 KW Neurotropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX
 OS Unidentified.

XX
 PN WO200292115-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 16-MAY-2002; 2002WO-CA000712.
 XX
 PR 16-MAY-2001; 2001US-0290971P.
 XX

XX (NYMO-) NYMOX CORP.
 XX
 PI Averbach PA;
 XX
 DR WPI; 2003-129234/12.
 XX

PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX

PS Claim 2; Page 45; 60pp; English.
 XX

CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC peptide of the invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

```

Db          11 HARL 14
|||||
RESULT 74
ABB81530
ID ABB81530 standard; peptide; 16 AA.
AC ABB81530;
XX
XX 02-SEP-2002 (first entry)
XX
XX Neural thread protein (NTP) peptide #20.
XX
XX Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;
KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
KW hypoxia; ischaemia; cerebral infarction.
XX
XX Homo sapiens.
OS
XX WO200234915-A2.
XX
XX 02-MAY-2002.
XX
XX 25-OCT-2001; 2001WO-US042813.
XX
XX 27-OCT-2000; 2000US-00697590.
XX
XX (NYMO-) NYMOX PHARM CORP.
XX
XX Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
XX
XX WPI; 2002-507998/54.
XX
XX New Harlil peptide sequences of the Neural Thread Protein, useful in
XX therapeutic assays, e.g. as targets for developing drugs for treating
XX Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
XX these diseases.
XX
XX Claim 3; Page 29; 53pp; English.
XX
XX The present invention describes a neural thread protein (NTP) peptide
XX having an amino acid sequence selected from ABB81511 to ABB81529 and
XX their homologues, which are referred collectively as Harlil peptides (I).
XX (I) have neuroprotective, neurotropic, vasotropic and cerebroprotective
XX activities, and can be used in peptide therapy. The Harlil peptide
XX sequences can be used as analogues for NTP in therapeutic or diagnostic
XX assays by replacing NTP with the peptide in such an assay. The Harlil
XX peptides are also useful as a trap material in a diagnostic or
XX therapeutic assay. Therefore, the Harlil peptides are useful in binding
XX assays, protein and antibody purification, therapeutics or diagnostics.
XX In particular, the peptides are also useful for diagnosing Alzheimer's
XX disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
XX glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
XX are also useful as targets for drug development for the treatment of
XX these diseases. The present sequence represents a specifically claimed
XX peptide from the present invention
XX
XX Sequence 16 AA;
XX
XX Query Match          100.0%; Score 21; DB 5; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 2.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy          1 HARL 4
XX          |||||
XX Db          2 HARL 5
XX
XX RESULT 75
XX ABB02984
XX ID ABB02984 standard; peptide; 16 AA.
XX
AC ABB02984;
XX
XX 20-JAN-2003 (first entry)
XX
XX Human neural thread protein AD7C-NTP, peptide fragment #4.
XX
XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
XX transplantation; grafting; chemotherapy; immunotherapy; vaccination;
XX ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
XX radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
XX malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
XX cosmetic modification; vascular disease; atherosclerosis;
XX arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
XX autoimmune disease; metabolic disease; traumatic disease;
XX physical injury; nutritional deficiency disease; infectious disease;
XX amyloid disease; fibrosis disease; storage disease;
XX congenital malformation; enzyme deficiency disease; poisoning;
XX intoxication; environmental disease; radiation disease;
XX endocrine disease; degenerative disease; mechanical disease.
XX
XX Homo sapiens.
OS
XX WO200297030-A2.
XX
XX 05-DEC-2002.
XX
XX 24-MAY-2002; 2002WO-CA000759.
XX
XX 25-MAY-2001; 2001US-0293156P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-041406/03.
XX
XX Novel peptides similar in amino acid sequence to neural thread proteins
XX (NTP), useful for treating unwanted cellular proliferations such as
XX malignant tumors and prostatic hyperplasia.
XX
XX Claim 3; Page 15; 78pp; English.
XX
XX The invention describes an NTP-peptide (I) comprising at least one amino
XX acid sequence corresponding to part of the amino acid sequence of a
XX neural thread protein, AD7C-NTP. The invention provides a method of
XX treating a condition requiring removal or destruction of cells of a
XX mammal comprising administering to a mammal, a therapeutic amount of (I).
XX The treatment is administered to the mammal before, during or after
XX surgical excision, transplantation, grafting, chemotherapy,
XX immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
XX laser therapy, phototherapy, gene therapy and/or radiation. The method is
XX useful for treatment of benign or malignant tumour; hyperplasia,
XX hypertrophy or overgrowth of tissue; virally, bacterially or
XX parasitically altered tissue; malformation of tissue selected from lung,
XX breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
XX sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
XX gland, blood, brain and its coverings, spinal cord, muscle, connective
XX tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
XX reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
XX tonsils, mouth and lymph nodes and lymphoid system; tonsillary
XX hyperplasia; prostatic hyperplasia; cosmetic modification to a tissue;
XX vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
XX varicose veins; inflammatory disease; autoimmune disease; metabolic
XX disease; hereditary/genetic disease; traumatic disease; physical injury;
XX nutritional deficiency disease; infectious disease; amyloid disease;
XX fibrosis disease; storage disease; congenital malformation; enzyme
XX deficiency disease; poisoning; intoxication; environmental disease;
XX radiation disease; endocrine disease; degenerative disease and mechanical
XX disease. This is the amino acid sequence of a human neural thread protein
XX AD7C-NTP peptide fragment
XX
XX Sequence 16 AA;

```

Query Match 100.0%; Score 21; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
 ||||
Db 4 HARL 7

Search completed: July 5, 2005, 16:32:36
Job time : 164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 5, 2005, 16:32:43 ; Search time 38 Seconds
(without alignments)
10.128 Million cell updates/sec

Title: US-09-697-590-2_COPY_292_295

Perfect score: 21
Sequence: 1 HARL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	44	2 B97644	hypothetical prote
2	21	100.0	59	2 B69101	hypothetical prote
3	21	100.0	65	2 S28481	ribQ protein - Vib
4	21	100.0	67	2 AF2590	hypothetical prote
5	21	100.0	71	2 B69337	hypothetical prote
6	21	100.0	74	2 C70501	hypothetical prote
7	21	100.0	75	2 T06193	chlorophyll a/b-bi
8	21	100.0	80	2 F82684	hypothetical prote
9	21	100.0	83	2 G84144	hypothetical prote
10	21	100.0	85	2 AH2622	conserved hypotet
11	21	100.0	85	2 H97404	hypothetical prote
12	21	100.0	93	2 E83358	hypothetical prote
13	21	100.0	93	2 T20227	hypothetical prote
14	21	100.0	96	2 S38916	hypothetical prote
15	21	100.0	100	2 A97833	hypothetical prote
16	21	100.0	101	2 C81012	conserved hypotet
17	21	100.0	103	2 A97484	hypothetical prote
18	21	100.0	103	2 A12701	hypothetical prote
19	21	100.0	103	2 D97412	hypothetical prote
20	21	100.0	106	2 S04786	mobilization prote
21	21	100.0	107	2 JQ0389	mobilization prote
22	21	100.0	107	2 T07540	hypothetical prote
23	21	100.0	108	2 S43154	diaminopimelate ep
24	21	100.0	116	1 QOCVB1	V2 protein - tomat
25	21	100.0	116	2 D49339	cell growth regula
26	21	100.0	116	2 I57506	oncogene tyrosine
27	21	100.0	118	2 I77386	hypothetical prote
28	21	100.0	119	2 E70718	hypothetical membr
29	21	100.0	120	2 C96008	

30	21	100.0	121	2 E87139	50S ribosomal prot
31	21	100.0	121	2 T37737	hypothetical prote
32	21	100.0	122	2 T45382	ribosomal protein
33	21	100.0	122	2 C81775	hypothetical prote
34	21	100.0	122	2 G81198	hypothetical prote
35	21	100.0	124	2 D85843	unknown protein en
36	21	100.0	124	2 F90822	probable tail asse
37	21	100.0	124	2 A90854	probable tail asse
38	21	100.0	124	2 E90876	probable tail asse
39	21	100.0	124	2 D85630	probable tail asse
40	21	100.0	124	2 B90909	probable tail asse
41	21	100.0	125	2 T45512	hypothetical prote
42	21	100.0	127	2 PC2265	cytochrome P450 pr
43	21	100.0	127	2 B91218	thioredoxin 1 (imp
44	21	100.0	127	2 C86064	thioredoxin 1 (imp
45	21	100.0	129	2 G72460	hypothetical prote
46	21	100.0	132	1 Q95C8	hypothetical prote
47	21	100.0	132	2 G84669	hypothetical prote
48	21	100.0	133	2 T07498	hypothetical prote
49	21	100.0	133	2 S72720	hypothetical prote
50	21	100.0	137	2 B83475	hypothetical prote
51	21	100.0	139	2 AF1925	hypothetical prote
52	21	100.0	140	2 D85681	hypothetical prote
53	21	100.0	140	2 AB2828	hypothetical prote
54	21	100.0	141	1 N12RAT	nitrogenase (EC 1.
55	21	100.0	142	2 AC1279	hypothetical prote
56	21	100.0	142	2 AC1642	hypothetical prote
57	21	100.0	143	2 T16332	hypothetical prote
58	21	100.0	144	2 B83069	hypothetical prote
59	21	100.0	145	2 AF2820	two component resp
60	21	100.0	145	2 F97598	hypothetical prote
61	21	100.0	145	2 B91252	hypothetical prote
62	21	100.0	149	2 T03477	potential phosphat
63	21	100.0	149	2 E95314	conserved hypotet
64	21	100.0	151	2 S72243	dynein heavy chain
65	21	100.0	152	2 S38247	hypothetical prote
66	21	100.0	155	2 T10014	hypothetical prote
67	21	100.0	155	2 A70700	hypothetical prote
68	21	100.0	157	2 AF0606	probable membrane
69	21	100.0	157	2 AH0999	probable membrane
70	21	100.0	157	2 D84243	hypothetical prote
71	21	100.0	159	2 AF3135	NADH dehydrogenase
72	21	100.0	160	2 T36282	probable tryptoph
73	21	100.0	160	2 AC2958	conserved hypotet
74	21	100.0	160	2 E96710	hypothetical prote
75	21	100.0	162	2 D82983	leucine-responsive
76	21	100.0	162	2 B87321	transcription regu
77	21	100.0	162	2 B64824	probable membrane
78	21	100.0	162	2 B90746	hypothetical prote
79	21	100.0	162	2 F85596	hypothetical prote
80	21	100.0	163	2 F70777	probable low molec
81	21	100.0	164	2 C98325	probable transcrip
82	21	100.0	169	2 S03593	regulatory protein
83	21	100.0	170	2 A75513	DNA topology modul
84	21	100.0	171	2 E98288	hypothetical prote
85	21	100.0	171	2 AE2995	hypothetical prote
86	21	100.0	172	2 AE3009	hypothetical prote
87	21	100.0	172	2 A96275	hypothetical prote
88	21	100.0	175	2 S57987	hypothetical prote
89	21	100.0	176	2 G87606	transcription regu
90	21	100.0	178	2 B83645	conserved hypotet
91	21	100.0	179	2 B75636	transcription regu
92	21	100.0	180	2 B7695	PTS system, nitrog
93	21	100.0	180	2 F82187	TonB system transp
94	21	100.0	181	2 E84337	histidine triad pr
95	21	100.0	182	2 PN0541	recombination prot
96	21	100.0	183	2 T18193	hypothetical prote
97	21	100.0	183	2 T17492	hypothetical prote
98	21	100.0	183	2 T29987	hypothetical prote
99	21	100.0	183	2 H83561	hypothetical prote
100	21	100.0	184	2 F98152	NAD-dependent form

ALIGNMENTS

```
RESULT 1
B97644
hypothetical protein AGR_C_4298 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium_tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97644
A:; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97644
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <KUR>
A:Cross-references: UNIPROT:Q8U546; GB:AE007869; PIDN:AAK88107.1; PID:gl5157539; GSPDB:C
C:Genetics:
A:Gene: AGR_C_4298
A:Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 12 HARL 15

RESULT 2
B69101
hypothetical protein MTH1750 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69101
A:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69101
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-59 <MTH>
A:Cross-references: UNIPROT:O27782; GB:AE000930; GB:AE000666; NID:g2622872; PIDN:AA8622
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1750

Query Match 100.0%; Score 21; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 15 HARL 18

RESULT 3
S28481
rfbQ protein - Vibrio cholerae (strain O17)
C:Species: Vibrio cholerae
A:Variety: strain O17
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28481
R;Manning, P.A.
submitted to the EMBL Data Library, May 1991
A:Reference number: S28467
A:Accession: S28481
```

```
A:Molecule type: DNA
A:Residues: 1-65 <MAN>
A:Cross-references: UNIPROT:Q07026; EMBL:X59554; NID:g48381; PIDN:CAA42147.1; PID:g4839
A:Experimental source: strain O17
C:Genetics:
A:Gene: rfbQ

Query Match 100.0%; Score 21; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 53 HARL 56

RESULT 4
AF2590
hypothetical protein Atu0115 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2590
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-67 <KUR>
A:Cross-references: UNIPROT:Q8UJ23; GB:AE008688; PIDN:AA41140.1; PID:gl7738435; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0115
A:Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 53 HARL 56

RESULT 5
B69337
hypothetical protein AF0698 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69337
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69337
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-71 <KLE>
A:Cross-references: UNIPROT:O29560; GB:AE001056; GB:AE000782; NID:g2689379; PIDN:AA8905

Query Match 100.0%; Score 21; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 HARL 4
 ||||
 Db 4 HARL 7

RESULT 6

C70501
 hypothetical protein Rv1684 - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: C70501
 R;Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: C70501
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-74 <COL>
 A;Cross-references: UNIPROT:O33186; GB:Z98268; GB:AL123456; NID:g3261839; PIDN:CAB10941
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: Rv1684

Query Match 100.0%; Score 21; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 61 HARL 64

RESULT 7

T06193
 chlorophyll a/b-binding protein - barley (fragment)
 C;Species: Hordeum vulgare (barley)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06193
 R;Humbeck, K.; Krupinska, K.
 submitted to the EMBL Data Library, May 1998
 A;Description: Differential regulation of chlorophyll a/b-binding proteins and ELIP in m
 A;Reference number: 215522
 A;Accession: T06193
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-75 <HUM>
 A;Cross-references: UNIPROT:O65817; EMBL:AJ006296; PIDN:CAA06961.1
 A;Experimental source: cv. Carina, leaf
 C;Genetics:
 A;Gene: CP29
 C;Superfamily: chlorophyll a/b-binding protein
 C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem II; thylakoi

Query Match 100.0%; Score 21; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 30 HARL 33

RESULT 8

F82684
 hypothetical protein XF1417 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: F82684
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: F82684
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <SIM>
 A;Cross-references: UNIPROT:Q9PDG2; GB:AE003972; GB:AE003849; NID:g9106418; PIDN:AAF842
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, A.; Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froi J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lali chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasir A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF1417

Query Match 100.0%; Score 21; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 53 HARL 56

RESULT 9

G84144
 hypothetical protein BH3959 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: G84144
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hii Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: G84144
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-83 <STO>
 A;Cross-references: UNIPROT:Q9K5X7; GB:AF001520; GB:BA000004; NID:g10176401; PIDN:BA807
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3959

Query Match 100.0%; Score 21; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 35 HARL 38

RESULT 10

AH2622
 conserved hypothetical protein Atu0376 [imported] - Agrobacterium tumefaciens (strain C
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AH2622
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel
 ; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C59.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q8UIC1; GB:AB008688; PIDN:AAL41398.1; PID:g17738716; GSPDB:G000023; CESP:C
C;Genetics:
A;Experimental source: strain C58 (Dupont)
A;Gene: Atu0376
A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 7 HARL 10

RESULT 11
H97404
hypothetical protein AGR_C_659 [imported] - *Agrobacterium tumefaciens* (strain C58, Cerevisiae)
C;Species: *Agrobacterium tumefaciens*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97404
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wallam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C59.
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H97404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q8UIC1; GB:AB007869; PIDN:AAK86193.1; PID:g15155290; GSPDB:G000023; CESP:C
C;Genetics:
A;Gene: AGR_C_659
A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 7 HARL 10

RESULT 12
E83358
hypothetical protein PA2292 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83358
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83358
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-93 <STO>
A;Cross-references: UNIPROT:Q91113; GB:AB004655; GB:AE004091; NID:G9948321; PIDN:AAG0568
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2292

Query Match 100.0%; Score 21; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 31 HARL 34

RESULT 13
T20227
hypothetical protein C54G10.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20227
R;Matthews, L. submitted to the EMBL Data Library, June 1996
A;Reference number: Z19240
A;Accession: T20227
A;Status: preliminary; translated from GB/EMBL/DDJ
A;Molecule type: DNA
A;Residues: 1-93 <WIL>
A;Cross-references: UNIPROT:Q18842; EMBL:Z75532; PIDN:CAA99809.1; GSPDB:GN00023; CESP:C
C;Genetics:
A;Experimental source: clone C54G10
A;Gene: CESP:C54G10.1
A;Map position: 5

Query Match 100.0%; Score 21; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 19 HARL 22

RESULT 14
S38916
hypothetical protein 4 - phage phi-C31
C;Species: phage phi-C31
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S38916
R;Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.F. submitted to the EMBL Data Library, November 1993
A;Reference number: S38912
A;Accession: S38916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <HAR>
A;Cross-references: UNIPROT:Q38025; EMBL:X76289; NID:g432610; PIDN:CAA53915.1; PID:g432

Query Match 100.0%; Score 21; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 82 HARL 85

RESULT 15
A97833
hypothetical protein RC1065 [imported] - *Rickettsia conorii* (strain Malish 7)
C;Species: *Rickettsia conorii*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97833
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: A97833

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <KUR>
A;Cross-references: UNIPROT:Q92GQ7; GB:AE006914; PIDN:AAL03603.1; PID:gl5620185; GSPDB:C
A;Gene: RC1065

Query Match 100.0%; Score 21; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 77 HARL 80

RESULT 16
C81012
conserved hypothetical protein NMB2058 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81012; G81953
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81012
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <TET>
A;Cross-references: UNIPROT:Q9JRG6; GB:AE002555; GB:AE002098; NID:G7227310; PIDN:AAE4237
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagele, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: G81953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:G7379120; PIDN:CAB83678.1; PID:G737913
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB2058; NMA0377

Query Match 100.0%; Score 21; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 12 HARL 15

RESULT 17
A97484
hypothetical protein AGR_C_1876 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97484
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97484
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KUR>

Query Match 100.0%; Score 21; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

A;Cross-references: UNIPROT:Q8UGL9; GB:AE007869; PIDN:AAK86826.1; PID:gl5156036; GSPDB:
C;Genetics:
A;Gene: AGR_C_1876
A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

RESULT 18
AI2701
hypothetical protein Atul018 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI2701
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KUR>
A;Cross-references: UNIPROT:Q8UGL9; GB:AE008688; PIDN:AAL42031.1; PID:gl7739407; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul018
A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

RESULT 19
D97412
hypothetical protein AGR_C_774 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97412
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KUR>
A;Cross-references: UNIPROT:Q8U5L6; GB:AE007869; PIDN:AAK86253.1; PID:gl5155361; GSPDB:
C;Genetics:
A;Gene: AGR_C_774
A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

Db 45 HARL 48

RESULT 20

S04786
mobilization protein mobC - Escherichia coli plasmid ColK
C;Species: Escherichia coli
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S04786
R;Boyd, A.C.; Archer, J.A.K.; Sherratt, D.J.
Mol. Gen. Genet. 217, 488-498, 1989
A;Title: Characterization of the ColEI mobilization region and its protein products.
A;Reference number: JQ0389; MUID:89364735; PMID:2671664
A;Accession: S04786
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-106 <BOY>
A;Cross-references: UNIPROT:O52992
C;Genetics:
A;Gene: mobC; mbkC
A;Genome: plasmid

Query Match 100.0%; Score 21; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 11 HARL 14

RESULT 21

JQ0389
mobilization protein mbec - Escherichia coli plasmid ColEI
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JQ0389
R;Boyd, A.C.; Archer, J.A.K.; Sherratt, D.J.
Mol. Gen. Genet. 217, 488-498, 1989
A;Title: Characterization of the ColEI mobilization region and its protein products.
A;Reference number: JQ0389; MUID:89364735; PMID:2671664
A;Accession: JQ0389
A;Molecule type: DNA
A;Residues: 1-107 <BOY>
A;Cross-references: UNIPROT:P13657; GB:X15873; NID:G45448; PIDN:CAA33882.1; PID:G45449
C;Genetics:
A;Gene: mbec
A;Genome: plasmid

Query Match 100.0%; Score 21; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 11 HARL 14

RESULT 22

T07540
hypothetical protein 107 - Japanese black pine chloroplast
C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07540
R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A;Reference number: Z16030; MUID:95024047; PMID:7937893
A;Accession: T07540
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-107 <WAK>
A;Cross-references: UNIPROT:Q32978; EMBL:D17510; NID:G529643; PIDN:BAA04416.1; PID:G1263

C;Genetics:

A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 100.0%; Score 21; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 75 HARL 78

RESULT 23

S43154
diaminopimelate epimerase (EC 5.1.1.7) - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S61400; S43154
R;Hofte, M.; Dong, Q.; Kourambas, S.; Krishnapillai, V.; Sherratt, D.; Mergeay, M.
Mol. Microbiol. 14, 1011-1020, 1994
A;Title: The ssb gene product, which affects pyoverdinin production in Pseudomonas aeruginosa
A;Reference number: S61400; MUID:95231283; PMID:7715441
A;Accession: S61400
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <HOE>
A;Cross-references: UNIPROT:Q51564; EMBL:X78478; NID:G468712; PIDN:CAA55224.1; PID:G468713
R;Hofte, M.; Dong, Q.; Kourambas, S.; Krishnapillai, V.; Mergeay, M.
submitted to the EMBL Data Library, March 1994
A;Description: The ssb gene product which affects pyoverdinin production in Pseudomonas aeruginosa
A;Reference number: S43154
A;Accession: S43154
A;Molecule type: DNA
A;Residues: 1-108 <HOF>
A;Cross-references: EMBL:X78478; NID:G468712; PIDN:CAA55224.1; PID:G468713
C;Genetics:
A;Gene: dapF
C;Superfamily: diaminopimelate epimerase
C;Keywords: isomerase; lysine biosynthesis

Query Match 100.0%; Score 21; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 35 HARL 38

RESULT 24

Q0CVB1
V2 protein - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E40779
R;Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A;Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single ORF
A;Reference number: A40779; MUID:92024070; PMID:1926771
A;Accession: E40779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-116 <NAV>
A;Cross-references: UNIPROT:P27269; GB:X15656; NID:G62204; PIDN:CAA33687.1; PID:G62206
C;Superfamily: tomato yellow leaf curl virus V2 protein

Query Match 100.0%; Score 21; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 65 HARL 68
|||||
RESULT 25
D49339
cell growth regulatory protein ChpB - Escherichia coli (strain K-12)
N/Alternate names: penk-like protein 2
C/Species: Escherichia coli
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: D49339; S56451; D65234
R/Maeda, Y.; Miyakawa, K.; Nishimura, Y.; Ohtsubo, E.
J. Bacteriol. 175, 6850-6856, 1993
A/Title: chpA and chpB, Escherichia coli chromosomal homologs of the pen locus responsible for penicillin resistance
A/Reference number: A49339; MUID:94042847; PMID:8226627
A/Accession: D49339
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-116 <MAS>
A/Cross-references: UNIPROT:P33647; GB:D16451; NID:G452513; PIDN:BA03920.1; PID:d100443
R/Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A/Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.0 to 92.1 Mb
A/Reference number: S56314; MUID:95334362; PMID:7610040
A/Accession: S56451
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-116 <BUR>
A/Cross-references: EMBL:U14003; NID:G1263172; PIDN:AA97122.1; PID:G537067
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97428617; PMID:9278503
A/Accession: D65234
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-116 <BLAT>
A/Cross-references: GB:AE000494; GB:U00096; NID:G1790670; PIDN:AAC77182.1; PID:G1790672
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: chpB
C/Keywords: DNA binding
Query Match 100.0%; Score 21; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
|||||
Db 89 HARL 92
RESULT 26
I57506
oncogene tyrosine protein kinase receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I57506
R/Coulier, F.; Kumar, R.; Ernst, M.; Klein, R.; Martin-Zanca, D.; Barbacid, M.
Mol. Cell. Biol. 10, 4202-4210, 1990
A/Title: Human trk oncogenes activated by point mutation, in-frame deletion, and duplication
A/Reference number: I57506; MUID:90318386; PMID:1695324
A/Accession: I57506
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-118 <RES>
A/Cross-references: UNIPROT:Q00182; GB:M55336; NID:G339913; PIDN:AAA36768.1; PID:G339914
C/Genetics:
A/Gene: trk2
Query Match 100.0%; Score 21; DB 2; Length 118;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
|||||
Db 7 HARL 10
RESULT 27
I77386
oncogene tyrosine protein kinase receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I77386
R/Coulier, F.; Kumar, R.; Ernst, M.; Klein, R.; Martin-Zanca, D.; Barbacid, M.
Mol. Cell. Biol. 10, 4202-4210, 1990
A/Title: Human trk oncogenes activated by point mutation, in-frame deletion, and duplication
A/Reference number: I57506; MUID:90318386; PMID:1695324
A/Accession: I77386
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-118 <RES>
A/Cross-references: UNIPROT:Q04227; GB:M55337; NID:G339915; PIDN:AAA36769.1; PID:G339916
C/Genetics:
A/Gene: trk4
Query Match 100.0%; Score 21; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
|||||
Db 7 HARL 10
RESULT 28
E70718
hypothetical protein RV0967 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: E70718
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A/Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: E70718
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-119 <COL>
A/Cross-references: UNIPROT:P71543; GB:279700; GB:AL123456; NID:G3261628; PIDN:CAB02009
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV0967
Query Match 100.0%; Score 21; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
|||||
Db 96 HARL 99
RESULT 29
C96008
hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: C96008
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna-

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C96008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120 <KUR>
A;Cross-references: UNIPROT:Q92U12; GB:AL591985; PIDN:CAC49731.1; PID:gl5141218; GSPDB:GN00066;
R;Galibert, F.; Finan, T.M.; Long, S.R.; Fulher, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb21501
A;Genome: plasmid

Query Match 100.0%; Score 21; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 84 HARL 87

RESULT 30

E87139
50S ribosomal protein L18 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: E87139
R;Cole, S.T.; Eiglmeter, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
eam, M.A.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: E87139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <STO>
A;Cross-references: GB:AL450380; NID:gl3093539; PIDN:CAC30797.1; GSPDB:GN00147
C;Genetics:
A;Gene: rplR
C;Superfamily: Escherichia coli ribosomal protein L18

Query Match 100.0%; Score 21; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 16 HARL 19

RESULT 31

T37737
hypothetical protein SPAC167.06c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37737; T38952
R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: 221743
A;Accession: T37737
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-121 <RIE>
A;Cross-references: UNIPROT:P97133; EMBL:AL035248; PIDN:CAA22851.1; GSPDB:GN00066; SPDB
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, May 1997
A;Reference number: 221819
A;Accession: T38952
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-121 <SKE>
A;Cross-references: EMBL:Z95396; PIDN:CAB08760.1; GSPDB:GN00066; SPDB:SPAC57A7.02c
C;Genetics:
A;Gene: SPAC57A7.02c; cosmid c57A7
A;Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 35 HARL 38

RESULT 32

T45382
ribosomal protein L18 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45382
R;Cole, S.T.; Fieselles, B.; Honore, N.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z22966
A;Accession: T45382
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-122 <COL>
A;Cross-references: UNIPROT:O32999; EMBL:Z98756; PIDN:CAB11452.1
A;Experimental source: cosmid B2492
C;Genetics:
A;Note: rplR
C;Superfamily: Escherichia coli ribosomal protein L18

Query Match 100.0%; Score 21; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 17 HARL 20

RESULT 33

C81775
hypothetical protein NMA2047 [imported] - Neisseria meningitidis (strain Z2491 serogrou
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: C81775
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: C81775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <PAR>
A;Cross-references: UNIPROT:Q9JTT10; GB:AL162759; NID:g7380672; PIDN:CAB8852
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2047

Query Match 100.0%; Score 21; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 76 HARL 79

RESULT 34
 G81198
 Hypothetical protein NMB0438 [imported] - Neisseria meningitidis (strain MC58 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: G81198
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: G81198
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-122 <TET>
 A;Cross-references: UNIPROT:Q9KOW8; GB:AE002400; GB:AE002098; NID:G7225659; PIDN:AAF4087
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0438

Query Match 100.0%; Score 21; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 76 HARL 79

RESULT 35
 D85843
 unknown protein encoded within prophage CP-933V [imported] - Escherichia coli (strain O1
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: D85843
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: D85843
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <STO>
 A;Cross-references: UNIPROT:Q8X5B6; GB:AE005174; NID:G12516372; PIDN:ANG57208.1; GSPDB:G
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z3320

Query Match 100.0%; Score 21; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 104 HARL 107

RESULT 36
 F90822
 Probable tail assembly chaperone [imported] - Escherichia coli (strain O157:H7, substrain

C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: F90822
 R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: F90822
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <HAY>
 A;Cross-references: UNIPROT:Q8X4K1; GB:BA000007; PIDN:BA834973.1; PID:G13361014; GSPDB:
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECe1550

Query Match 100.0%; Score 21; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 104 HARL 107

RESULT 37
 A90854
 Probable tail assembly chaperone [imported] - Escherichia coli (strain O157:H7, substrain
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: A90854
 R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: A90854
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <HAY>
 A;Cross-references: UNIPROT:Q8X4K1; GB:BA000007; PIDN:BA835224.1; PID:G13361266; GSPDB:
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECe1801

Query Match 100.0%; Score 21; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 104 HARL 107

RESULT 38
 E90876
 Probable tail assembly chaperone [imported] - Escherichia coli (strain O157:H7, substrain
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: E90876
 R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: E90876
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <HAY>
 A;Cross-references: UNIPROT:Q8X5B6; GB:BA000007; PIDN:BA835404.1; PID:G13361446; GSPDB:
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:

A;Gene: ECs1981

Query Match 100.0%; Score 21; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
Db 104 HARL 107

RESULT 39

D85630
probable tail assembly chaperone [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85630
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: D85630

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-124 <STO>

A;Cross-references: UNIPROT:Q8X5B6; GB:AE005174; NID:g12514215; PIDN:AAG55504.1; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z1371

Query Match 100.0%; Score 21; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
Db 104 HARL 107

RESULT 40

B90909
probable tail assembly chaperone [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B90909
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B90909

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-124 <HAY>

A;Cross-references: UNIPROT:Q8XAH6; GB:BA000007; PIDN:BA35665.1; PID:g13361708; GSPDB:C
A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs2242

Query Match 100.0%; Score 21; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
Db 104 HARL 107

RESULT 41

T49512

hypothetical protein B14D6.640 [imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49512

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49512

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-125 <SCH>

A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.640

A;Experimental source: BAC clone B14D6; strain OR74A

C;Genetics:

A;Gene: NCSP:B14D6.640

A;Map position: 6

C;Superfamily: Neurospora crassa hypothetical protein B14D6.640

Query Match 100.0%; Score 21; DB 2; Length 125;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
Db 11 HARL 14

RESULT 42

PC2265

cytochrome P450 protein, CYP4H5 - Anopheles albimanus (fragment)

C;Species: Anopheles albimanus

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C;Accession: PC2265

R;Scott, J.A.; Collins, F.H.; Feverisen, R.

Biochem. Biophys. Res. Commun. 205, 1452-1459, 1994

A;Title: Diversity of cytochrome P450 genes in the mosquito, Anopheles albimanus.

A;Reference number: PC2257; MUID:95100981; PMID:7545968

A;Accession: PC2265

A;Molecule type: DNA

A;Residues: 1-127 <SCO>

A;Cross-references: UNIPROT:Q16911; GB:L38686; NID:g605609; PIDN:AAA65831.1; PID:g60561

C;Genetics:

A;Gene: CYP4H5

C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C;Keywords: heme

Query Match 100.0%; Score 21; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
Db 41 HARL 44

RESULT 43

B91218

thioredoxin 1 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004

C;Accession: B91218

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B91218

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-127 <HAY>

A;Cross-references: GB:BA000007; PIDN:BA38137.1; PID:g13364189; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs4714

C;Superfamily: Thioredoxin; thioredoxin homology

Query Match 100.0%; Score 21; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 9 HARL 12

RESULT 44

C86064
 thioredoxin 1 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
 C;Accession: C86064
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: C86064
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-127 <STO>
 A;Cross-references: GB:AB005174; NID:G12518641; PIDN:AA058975.1; GSPDB:GN00145; UWGP:Z52
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: trxA
 C;Superfamily: Thioredoxin; thioredoxin homology

Query Match 100.0%; Score 21; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 9 HARL 12

RESULT 45

G72460
 hypothetical protein APE2331 - Aeropyrum pernix (strain KI)

C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: G72460
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: G72460
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-129 <KAW>
 A;Cross-references: UNIPROT:Q9Y9F7; DBJ:AP000064; NID:G5105945; PIDN:BA081343.1; PID:dl
 A;Experimental source: strain KI
 C;Genetics:
 A;Gene: APE2331

Query Match 100.0%; Score 21; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 44 HARL 47

RESULT 46

Q0EC8

hypothetical protein D-132 - Escherichia coli plasmid pBR322

C;Species: Escherichia coli

C;Date: 31-Dec-1980 #sequence_revision 31-Dec-1980 #text_change 09-Jul-2004

C;Accession: A04481
 R;Sutcliffe, J.G.
 Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
 A;Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
 A;Reference number: A90923; MUID:80002802; PMID:383387

A;Accession: A04481
 A;Molecule type: DNA
 A;Residues: 1-132 <SUT>
 A;Cross-references: UNIPROT:P03852
 C;Genetics:

A;Genome: plasmid
 C;Superfamily: Escherichia coli plasmid pBR322 hypothetical 15.3K protein

Query Match 100.0%; Score 21; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 32 HARL 35

RESULT 47

G84669

hypothetical protein At2g27180 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84669

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84669

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: UNIPROT:Q9SHT0; GB:AE002093; NID:G4646220; PIDN:AA026886.1; GSPDB:G

C;Genetics:

A;Gene: At2g27180

A;Map position: 2

Query Match 100.0%; Score 21; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 ||||
 Db 75 HARL 78

RESULT 48

T07498

hypothetical protein 133 - Japanese black pine chloroplast

C;Species: chloroplast Pinus thunbergiana (Japanese black pine)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C;Accession: T07498

R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiyama, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994

A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genom

A;Reference number: Z16030; MUID:95024047; PMID:7937893

A;Accession: T07498

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-133 <WAK>

A;Cross-references: UNIPROT:Q32960; EMBL:D17510; NID:G529643; PIDN:BA04376.1; PID:G126

C;Genetics:

A;Genome: chloroplast

C;Superfamily: Japanese black pine chloroplast hypothetical protein 133

C;Keywords: chloroplast

```
Query Match      100.0%; Score 21; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
    ||||
Db 94 HARL 97

RESULT 49
S72720
B1177 Cl 147 protein - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72720
R:Smith, D.R.; Robinson, K.
A:Submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B1177.
A:Reference number: S72694
A:Accession: S72720
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <SMI>
A:Cross-references: UNIPROT:Q49636; EMBL:U00011; NID:G466807; PIDN:AAAL7084.1; PID:G4668
C:Genetics:
A:Start codon: GTG

Query Match      100.0%; Score 21; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
    ||||
Db 116 HARL 119

RESULT 50
B83475
hypothetical protein PA1353 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83475
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
A:Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83475
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <STO>
A:Cross-references: UNIPROT:Q9I321; GB:AE004565; GB:AE004091; NID:G9947294; PIDN:AAG0474
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA1353

Query Match      100.0%; Score 21; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
    ||||
Db 53 HARL 56

RESULT 51
AF1925
hypothetical protein alr0953 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF1925
```

```
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguch
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Rep. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1925
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-139 <KOR>
A:Cross-references: UNIPROT:Q8YY98; GB:BA000019; PIDN:BAE72910.1; PID:gl7130299; GSPDB:
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0953

Query Match      100.0%; Score 21; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
    ||||
Db 60 HARL 63

RESULT 52
D85681
hypothetical protein Z1812 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85681
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85681
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <STO>
A:Cross-references: UNIPROT:Q8X3R7; GB:AE005174; NID:gl2514728; PIDN:AG55912.1; GSPDB:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1812

Query Match      100.0%; Score 21; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
    ||||
Db 120 HARL 123

RESULT 53
AB2828
hypothetical protein Atu2048 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB2828
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB2828
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <KUR>
A:Cross-references: UNIPROT:Q8UDS2; GB:AE008688; PIDN:AAL43040.1; PID:gl7740505; GSPDB:
A:Experimental source: strain C58 (Dupont)
C:Genetics:
```

A:Gene: Atu2048

A:Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||

Db 26 HARL 29

RESULT 54

NIZRAT

nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Rhizobium leguminosarum

N:Alternate names: dinitrogenase alpha chain; nitrogenase, component I alpha chain

C:Species: Rhizobium leguminosarum bv. trifolii

C:Date: 14-Nov-1993 #sequence_revision 14-Nov-1993 #text_change 09-Jul-2004

C:Accession: A00543

R:Scott, K.F.; Rolfe, B.G.; Shine, J.

DNA 2, 149-155, 1983

A:Title: Biological nitrogen fixation: primary structure of the Rhizobium trifolii iron

A:Reference number: A90942; MUID:83261209; PMID:6307623

A:Accession: A00543

A:Molecule type: DNA

A:Residues: 1-141 <SCO>

A:Cross-references: UNIPROT:P00465

A:Experimental source: strain SU329

C:Comment: The key enzymatic reactions in nitrogen fixation are catalyzed by the nitrogen

d the molybdenum-iron protein, which is a tetramer of two alpha and two beta chains that

C:Genetics:

A:Gene: nifD

C:Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain

C:Keywords: 4Fe-4S; ATP; iron; iron-sulfur protein; metalloprotein; molybdenum; nitrogen

F;17-141/Domain: nitrogenase vanadium-iron protein alpha chain homology (fragment) <VIA>

F;72,98/Binding site: 4Fe-4S cluster 1 (Cys) (covalent) #status predicted

F;98/Binding site: 4Fe-4S cluster 2 (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 21; DB 1; Length 141;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||

Db 12 HARL 15

RESULT 55

AC1279

hypothetical protein lm01635 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AC1279

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krift, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1279

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <GLA>

A:Cross-references: UNIPROT:Q8Y6P9; GB:NC_003210; PIDN:CAC99713.1; PID:gl6411071; GSPDB:

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lm01635

Query Match

Best Local Similarity 100.0%; Score 21; DB 2; Length 142;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||

Db 54 HARL 57

RESULT 56

AC1642

hypothetical protein homolog lin1676 [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AC1642

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krift, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; P

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1642

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <GLA>

A:Cross-references: UNIPROT:Q92B74; GB:AL592022; PIDN:CAC96907.1; PID:gl64114163; GSPDB

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin1676

Query Match

Best Local Similarity 100.0%; Score 21; DB 2; Length 142;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||

Db 54 HARL 57

RESULT 57

T16332

hypothetical protein F41G3.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16332

R:Menezes, S.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F41G3.

A:Reference number: Z18496

A:Accession: T16332

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-143 <MEN>

A:Cross-references: UNIPROT:Q20291; EMBL:U39999; NID:gl055133; PID:gl055138; PIDN:AAA81

C:Genetics:

A:Gene: CESP:F41G3.4

A:Introns: 17/3; 54/1; 80/3

Query Match

Best Local Similarity 100.0%; Score 21; DB 2; Length 143;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||

Db 76 HARL 79

RESULT 58

B83069

hypothetical protein PA4610 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: B83069

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <STO>
A;Cross-references: UNIPROT:Q9HV10; GB:AB004875; GB:AB004091; NID:99950857; PIDN:AAG0799
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4610

Query Match 100.0%; Score 21; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 100 HARL 103

RESULT 59
AF2820
two component response regulator Atu1985 [imported] - *Agrobacterium tumefaciens* (strain
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Accession: AF2820
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, F.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2820
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <KUR>
A;Cross-references: UNIPROT:Q8UDY1; GB:AB008688; PIDN:AAL42980.1; PID:g17740440; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1985
A;Map position: circular chromosome
C;Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon

Query Match 100.0%; Score 21; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 19 HARL 22

RESULT 60
F97598
hypothetical protein AGR_C3613 [imported] - *Agrobacterium tumefaciens* (strain C58, Cere
C;Species: *Agrobacterium tumefaciens*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
C;Accession: F97598
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <KUR>
A;Cross-references: UNIPROT:Q8UDY1; GB:AB007869; PIDN:AAK87743.1; PID:g15157110; GSPDB:G

C;Genetics:
A;Gene: AGR_C3613
A;Map position: circular chromosome
C;Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon

Query Match 100.0%; Score 21; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 19 HARL 22

RESULT 61
B91252
hypothetical protein ECs4986 [imported] - *Escherichia coli* (strain O157:H7, substrain R
C;Species: *Escherichia coli*
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B91252
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <HAY>
A;Cross-references: UNIPROT:Q8X2X8; GB:BA000007; PIDN:BA838409.1; PID:g13364462; GSPDB:G
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs4986
C;Superfamily: Haemophilus influenzae hypothetical protein HI1519

Query Match 100.0%; Score 21; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 117 HARL 120

RESULT 62
T03477
potential phosphate regulatory protein - *Rhodobacter capsulatus*
C;Species: *Rhodobacter capsulatus*
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03477
R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A>Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SB100
A;Reference number: Z14955; MUID:9740404; PMID:9256491
A;Accession: T03477
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-149 <VLC>
A;Cross-references: UNIPROT:O68044; EMBL:AF010496; NID:g3128256; PIDN:AAC16130.1; PID:g
C;Genetics:
A;Map position: 1
C;Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon
F;23-140/Domain: response regulator homology <RRH>

Query Match 100.0%; Score 21; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 53 HARL 56

RESULT 63
E95314
conserved hypothetical protein Sma0781 [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95314
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe,
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: E95314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <KUR>
A:Cross-references: UNIPROT:Q925W8; GB:AE006469; PIDN:AAK65079.1; PID:G14523514; GSPDB:C
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0781
A:Genome: plasmid

Query Match 100.0%; Score 21; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 127 HARL 130

RESULT 64
S72243
dynein heavy chain 5 - Chlamydomonas reinhardtii (fragment)
C:Species: Chlamydomonas reinhardtii
C:Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: S72243
R:Porter, M.E.; Knott, J.A.; Myster, S.H.; Farlow, S.J.
Genetics 144, 569-585, 1996
A:Title: The dynein gene family in Chlamydomonas reinhardtii.
A:Reference number: S72239; MUID:97044450; PMID:8889521
A:Accession: S72243
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-151 <FOR>
A:Cross-references: UNIPROT:Q96392; EMBL:U61368; NID:G1663743; PIDN:AAC49518.1; PID:G166
C:Genetics:
A:Introns: 78/3

Query Match 100.0%; Score 21; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 122 HARL 125

RESULT 65
S38247
hypothetical protein - Coxiella burnetii
C:Species: Coxiella burnetii
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S38247
R:Thiele, D.; Willems, H.; Haas, M.; Krauss, H.

Query Match 100.0%; Score 21; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

submitted to the EMBL Data Library, October 1993

A:Reference number: S38215

A:Accession: S38247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-152 <THI>

A:Cross-references: UNIPROT:Q45954; EMBL:X75356; NID:G407370; PIDN:CAA53135.1; PID:G580

C:Genetics:

A:Start codon: GTG

Query Match 100.0%; Score 21; DB 2; Length 152;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 95 HARL 98

RESULT 66

T10014

hypothetical protein - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T10014

R:Cole, S.T.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z16916

A:Accession: T10014

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-155 <COL>

A:Cross-references: UNIPROT:Q50189; EMBL:Z70722

C:Genetics:

A:Note: M51770.14c

C:Superfamily: Streptomyces coelicolor hypothetical protein SCH69.14

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

RESULT 67

A70700

hypothetical protein Rv0019c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70700

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70700

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-155 <COL>

A:Cross-references: UNIPROT:P71589; GB:Z80233; GB:AL123456; NID:G3261645; PIDN:CAB02439

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv0019c

C:Superfamily: Streptomyces coelicolor hypothetical protein SCH69.14

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy 1 HARL 4
|||||
Db 104 HARL 107

RESULT 68

AF0606
probable membrane protein STV0914 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0606
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05320.1; PID:gl6502084; GSPDB:GN00176
C;Genetics:
A;Gene: STV0914
C;Superfamily: Escherichia coli probable membrane protein ybjo

Query Match 100.0%; Score 21; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 11 HARL 14

RESULT 69

AH0999
probable membrane protein yrfB [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0999
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08124.1; PID:gl6505103; GSPDB:GN00176
C;Genetics:
A;Gene: yrfB

Query Match 100.0%; Score 21; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 47 HARL 50

RESULT 70

D84243
hypothetical protein Vng0868h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: D84243

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <STO>
A;Cross-references: UNIPROT:Q9HR46; GB:AE004437; NID:gl0580432; PIDN:AAG19312.1; GSPDB: C;Genetics:
A;Gene: VNG0868H

Query Match 100.0%; Score 21; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 24 HARL 27

RESULT 71

AF3135
NADH dehydrogenase I chain E nuoE [imported] - Agrobacterium tumefaciens (strain C58, D C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF3135
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3135
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <KUR>
A;Cross-references: UNIPROT:Q8U6V0; GB:AE008689; PIDN:AAL45500.1; PID:gl7743209; GSPDB: C;Genetics:
A;Gene: nuoE
A;Map position: linear chromosome

Query Match 100.0%; Score 21; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 142 HARL 145

RESULT 72

T36282
probable tryptophanyl-L-tryptophan synthetase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36282
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T36282
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-160 <MUR>
A;Cross-references: UNIPROT:Q8CJX0; EMBL:AL079345; PIDN:CAB45368.1; GSPDB:GN00070; SCORE A;Experimental source: strain A3(2)

C:Genetics:
A:Gene: trpS; SCOEDB:SCE68.32
C:Superfamily: tryptophan-trNA ligase

Query Match 100.0%; Score 21; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 87 HARL 90

RESULT 73

AC2958
conserved hypothetical protein Atu3265 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC2958
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2958
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <KUR>
A:Cross-references: UNIPROT:Q8UAV2; GB:AE008689; PIDN:AAL44081.1; PID:gi7741646; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3265
A:Map position: linear chromosome

Query Match 100.0%; Score 21; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 72 HARL 75

RESULT 74

E96710
hypothetical protein F24J5.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96710
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96710
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <STO>
A:Cross-references: UNIPROT:Q9SX24; GB:AE005173; NID:G5734716; PIDN:AAD49981.1; GSPDB:GN

Qy 1 HARL 4
Db 72 HARL 75

Qy 1 HARL 4
Db 72 HARL 75

Query Match

100.0%; Score 21; DB 2; Length 160;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 139 HARL 142

RESULT 75

D82983
leucine-responsive regulatory protein PA5308 [imported] - Pseudomonas aeruginosa (strain C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D82983
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Eadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lior, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D82983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <STO>
A:Cross-references: UNIPROT:Q9HTP6; GB:AE004943; GB:AE004091; NID:G9951615; PIDN:AAG086
A:Experimental source: strain PA01
C:Genetics:
A:Gene: lrp; PA5308
C:Superfamily: regulatory protein asnC

Query Match 100.0%; Score 21; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

Search completed: July 5, 2005, 16:48:02
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 5, 2005, 16:25:32 ; Search time 167 Seconds

(without alignments)
12.265 Million cell updates/sec

Title: US-09-697-590-2_COPY_292_295

Perfect score: 21

Sequence: 1 HARL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	31	2	Q9115 enterococcu
2	21	100.0	32	2	Q854D5 mycobacteri
3	21	100.0	37	2	Q9BQ22 homo sapien
4	21	100.0	37	2	Q7UDP8 shigella fl
5	21	100.0	39	2	Q7MZC6 photorhabdu
6	21	100.0	39	2	Q91W57 borna disea
7	21	100.0	42	2	Q9SQ83 arabidopsis
8	21	100.0	44	2	Q8U546 agrobacteri
9	21	100.0	45	2	Q8Y1N1 ralstonia s
10	21	100.0	46	2	Q8L6P5 gossypium h
11	21	100.0	51	2	Q7QP13 giardia lam
12	21	100.0	51	2	Q7UK71 rhodopirell
13	21	100.0	52	2	Q97152 drosophila
14	21	100.0	52	2	Q6GVJ3 burkholderi
15	21	100.0	57	2	Q8XUV9 ralstonia s
16	21	100.0	59	2	Q27782 methanobact
17	21	100.0	61	2	Q8NWM0 staphylococ
18	21	100.0	62	2	Q69SF4 oryza sativ
19	21	100.0	64	2	Q7XZX7 oryza sativ
20	21	100.0	65	2	Q07026 vibrio chol
21	21	100.0	66	2	Q63JV7 burkholderi
22	21	100.0	67	2	Q8UJ23 agrobacteri
23	21	100.0	67	2	Q6MX20 mycobacteri
24	21	100.0	67	2	Q7TXG9 mycobacteri
25	21	100.0	68	2	Q82PY5 streptomyce
26	21	100.0	68	2	Q8VAB5 white spot
27	21	100.0	70	2	Q943U1 oryza sativ
28	21	100.0	71	1	Y698_ARCFU
29	21	100.0	71	2	Q740G1 mycobacteri
30	21	100.0	72	2	Q8G1M5 brucella su
31	21	100.0	73	2	Q6Z3U0 oryza sativ

32	21	100.0	73	2	Q7UH15	Q7uh15 rhodopirell
33	21	100.0	73	2	Q89BQ6	Q89bq6 bradyrhizob
34	21	100.0	74	2	Q6WL03	Q6wl03 sus scrofa
35	21	100.0	74	2	Q84YV8	Q84yv8 oryza sativ
36	21	100.0	74	2	Q33186	Q33186 mycobacteri
37	21	100.0	74	2	Q7TZS8	Q7tzs8 mycobacteri
38	21	100.0	74	2	Q9IK63	Q9ik63 tt virus. o
39	21	100.0	75	2	Q85JV7	Q85jv7 perga conde
40	21	100.0	75	2	Q65817	Q65817 hordeum vul
41	21	100.0	76	2	Q70WA2	Q70wa2 acetobacter
42	21	100.0	78	2	Q88YS2	Q88ys2 lactobacill
43	21	100.0	79	2	Q7R3N8	Q7r3n8 giardia lam
44	21	100.0	79	2	Q6KIW8	Q6kiw8 oryza sativ
45	21	100.0	79	2	Q9XB07	Q9xb07 myxococcus
46	21	100.0	79	2	Q89NV1	Q89nv1 bradyrhizob
47	21	100.0	80	2	Q841N1	Q841n1 legionella
48	21	100.0	80	2	Q8XYV7	Q8xyv7 ralstonia s
49	21	100.0	80	2	Q9PDG2	Q9pdg2 xylella fas
50	21	100.0	81	2	Q9MG75	Q9mg75 cucumis mel
51	21	100.0	82	2	Q67W97	Q67w97 oryza sativ
52	21	100.0	82	2	Q71IA9	Q71ia9 lactobacill
53	21	100.0	82	2	Q821B6	Q821b6 ehigella fl
54	21	100.0	83	1	CI15_HUMAN	Q8buu7 homo sapien
55	21	100.0	83	1	CI15_MOUSE	Q86074 canine herp
56	21	100.0	83	1	Q9K5X7	Q9k5x7 bacillus ha
57	21	100.0	83	2	Q9WGD5	Q9wgd5 human papil
58	21	100.0	84	2	Q83X83	Q83x83 streptomyce
59	21	100.0	85	2	Q8D434	Q8d434 vibrio vuln
60	21	100.0	85	2	Q8UIC1	Q8uic1 agrobacteri
61	21	100.0	85	2	Q66074	Q66074 canine herp
62	21	100.0	86	2	Q649W2	Q649w2 uncultured
63	21	100.0	87	2	Q9FD17	Q9fd17 streptomyce
64	21	100.0	87	2	Q8PDJ9	Q8pdj9 xanthomonas
65	21	100.0	87	2	Q9FBZ3	Q9fbz3 streptomyce
66	21	100.0	88	2	Q9YKDS	Q9ykd5 tomato yell
67	21	100.0	89	2	Q73SS2	Q73ss2 mycobacteri
68	21	100.0	89	2	Q7PIL8	Q7pil8 chromobacte
69	21	100.0	89	2	Q7TM11	Q7tm11 uncultured
70	21	100.0	92	2	Q93SB6	Q93sb6 frankia sp.
71	21	100.0	93	1	VP44_BPAPS	Q81q4 bacterioph
72	21	100.0	93	2	Q18842	Q18842 caenorhabdi
73	21	100.0	93	2	Q11113	Q11113 pseudomonas
74	21	100.0	94	2	Q88UQ7	Q88uq7 lactobacill
75	21	100.0	95	2	P83814	P83814 thermus the
76	21	100.0	95	2	Q8ZK19	Q8zk19 salmonella
77	21	100.0	95	2	Q721A7	Q721a7 thermus the
78	21	100.0	95	2	Q8FRQ7	Q8frq7 corynebacte
79	21	100.0	96	2	Q38025	Q38025 bacterioph
80	21	100.0	96	2	Q8LG60	Q8lg60 arabidopsis
81	21	100.0	96	2	Q64TU0	Q64tu0 bacteroides
82	21	100.0	97	2	Q9M9M0	Q9m9m0 arabidopsis
83	21	100.0	97	2	Q7UNC8	Q7unc8 rhodopirell
84	21	100.0	98	2	Q75G68	Q75g68 oryza sativ
85	21	100.0	98	2	Q64RP8	Q64rp8 bacteroides
86	21	100.0	98	2	Q7UDF3	Q7udf3 shigella fl
87	21	100.0	99	2	Q87620	Q87620 pseudomonas
88	21	100.0	100	2	Q69W94	Q69w94 oryza sativ
89	21	100.0	100	2	Q92GQ7	Q92gq7 rickettsia
90	21	100.0	100	2	Q72GP3	Q72gp3 thermus the
91	21	100.0	100	2	Q678F4	Q678f4 lymphocysti
92	21	100.0	100	2	Q6LAG1	Q6lag1 pepper leaf
93	21	100.0	101	2	Q93U17	Q93u17 bacteroides
94	21	100.0	101	2	Q7DD48	Q7dd48 neisseria m
95	21	100.0	101	2	Q89Z80	Q89z80 bacteroides
96	21	100.0	101	2	Q9JRG6	Q9jrg6 neisseria m
97	21	100.0	102	2	Q6N8F4	Q6n8f4 rhodopsu
98	21	100.0	102	2	Q37880	Q37880 tomato yell
99	21	100.0	103	2	Q8GHI7	Q8ghi7 pigmentipha
100	21	100.0	103	2	Q8U5L6	Q8u5l6 agrobacteri

ALIGNMENTS

```
RESULT 1
ID Q9FI15 PRELIMINARY; PRT; 31 AA.
AC Q9FI15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein EP0010.
GN Name=EP0010;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Plasmid pAM373.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453452; PubMed=10998165;
RA De Boever E.H., Clewell D.B., Fraser C.M.;
RT "Enterococcus faecalis conjugative plasmid pAM373: complete nucleotide
sequence and genetic analyses of sex pheromone response.";
RL Mol. Microbiol. 37:1327-1341(2000).
DR EMBL; AE002565; AAG40421.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 31 AA; 3509 MW; 4E19CB94B3DB9421 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 12 HARL 15

RESULT 2
ID Q854D5 PRELIMINARY; PRT; 32 AA.
AC Q854D5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp132a.
GN Name=132a;
OS Mycobacteriophage Omega.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Fannunzio N.R.,
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AY129338; AAN12773.1; -.
SQ SEQUENCE 32 AA; 3523 MW; 43C968104E0B3FA8 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 14 HARL 17

RESULT 3
ID Q9BQ22 PRELIMINARY; PRT; 37 AA.
AC Q9BQ22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-2-macroglobulin (Fragment).
GN Name=A2M;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Teich N., Mossner J., Keim V.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21913005; PubMed=11916201;
RA Teich N., Walther K., Bodeker H., Mossner J., Keim V.;
RT "Relevance of variants in serum antiproteases for the course of
chronic pancreatitis.";
RL Scand. J. Gastroenterol. 37:360-365(2002).
DR EMBL; AF349032; AAK38109.1; -.
DR EMBL; AF349033; AAK38110.1; -.
DR GO; GO:0004866; F:endoropeptidase inhibitor activity; IEA.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4390 MW; AFE1C0124ACBF415 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 8 HARL 11

RESULT 4
ID Q7UDP8 PRELIMINARY; PRT; 37 AA.
AC Q7UDP8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=S0212;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=2457T;
RL MEDLINE=22590274; PubMed=12704152;
DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016978; AAP15745.1; -.
KW Hypothetical protein.
SQ SEQUENCE 37 AA; 3964 MW; 54EDAF9D68DD3F57 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 12 HARL 15
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RESULT 5
Q7MZC6 PRELIMINARY; PRT; 39 AA.
AC Q7MZC6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarities with bacteriophage protein.
GN OrderedLocusNames=plu4366;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Tacurit S., Bocs S., Bouraux-Eude C., Chandel M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boenare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571873; CAB16738.1; -.
DR PhotolList; plu4366; -.
KW Complete proteome.
SQ SEQUENCE 39 AA; 4480 MW; 5E0EC38FAB8C38CB CRC64;

Query Match 100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 32 HARL 35

RESULT 6
Q9IW57 PRELIMINARY; PRT; 39 AA.
AC Q9IW57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Glycoprotein (Fragment).
GN Name=gp57;
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ratBDV;
RX MEDLINE=20086018; PubMed=10622306; DOI=10.1016/S0140-6736(99)04703-0;
RA Schwenmle M., Jehle C., Formella S., Staeheli P.;
RT "Sequence similarities between human Bornavirus isolates and
RT laboratory strains question their human origin."
RL Lancet 354:1973-1974(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ratBDV;
RA Schwenmle M., Jehle C., Formella S., Staeheli P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250179; CAB87242.1; -.
FT NON TER 39
SQ SEQUENCE 39 AA; 4205 MW; D5A828ED9C2EF134 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HARL 4
DB 4 HARL 7

RESULT 7
Q9SQ83 PRELIMINARY; PRT; 42 AA.
ID Q9SQ83;
AC Q9SQ83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE R2R3-MYB protein (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=flower;
RA Rabinowicz P.D., Roberts C., Grotewold E.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 Myb-like domain.
DR EMBL; AF101050; AAF00581.1; -.
DR HSP; P06876; IMBK.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR009057; Homeodomain-like.
DR InterPro; IPR001005; Myb DNA binding.
DR Pfam; PF00249; Myb DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
FT NON TER 42
SQ SEQUENCE 42 AA; 4919 MW; 4CB2418E68408816 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 25 HARL 28

RESULT 8
Q8U546 PRELIMINARY; PRT; 44 AA.
ID Q8U546;
AC Q8U546;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AGR C 4298p.
GN OrderedLocusNames=AGR_C_4298;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
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RL Science 294:2323-2328(2001).
DR EMBL: AE008151; AAK88107.1; -.
DR PIR: B97644; B97644.
SQ SEQUENCE 44 AA; 4868 MW; B29035AD358B6A8C CRC64;

Query Match 100.0%; Score 21; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 12 HARL 15

RESULT 9
QBYINI PRELIMINARY; PRT; 45 AA.
AC QBYINI
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PUTATIVE FILIN PROTEIN.
GN Name=RS01563; OrderedLocuNames=RS0659;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RA MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646060; CAD14189.1; -.
KW Complete proteome.
SQ SEQUENCE 45 AA; 4776 MW; 9C76F7F9D65B3F05 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 12 HARL 15

RESULT 10
Q8L6P5 PRELIMINARY; PRT; 46 AA.
AC Q8L6P5
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB127 protein (Fragment).
GN Name=myb127;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22941922; PubMed=14580676; DOI=10.1016/j.bbexp.2003.08.009;
RA Suo J., Liang X., Pu L., Zhang Y., Xue Y.;
RT "Identification of GhMYB109 encoding a R2R3 MYB transcription factor
RT that expressed specifically in fiber initials and elongating fibers of
cotton (Gossypium hirsutum L.).";
RL Biochim. Biophys. Acta 1630:25-34(2003).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 Myb-like domain.
DR EMBL: AJ459156; CAD30605.1; -.
DR HSSP: P06876; 1GV2.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR009057; Homeodomain like.
DR InterPro: IPR001005; Myb_DNA_binding.
DR Pfam: PF00249; Myb_DNA-binding; 1.
DR PROSITE: PS0090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5296 MW; 4A7235042E02E5D6 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 29 HARL 32

RESULT 11
Q7QP13 PRELIMINARY; PRT; 51 AA.
AC Q7QP13
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP_83_11596.1141.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB01000181; EAA36747.1; -.
SQ SEQUENCE 51 AA; 5957 MW; 77A8A64D2875C6E9 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 2 HARL 5

RESULT 12
Q7UK71 PRELIMINARY; PRT; 51 AA.
AC Q7UK71
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=RB10821;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]

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RP SEQUENCE FROM N.A.
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schleimer H., Amann R., Reinhardt R.,
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.",
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294152; CAD77010.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 51 AA; 5642 MW; FCE6166138B5CB09 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 42 HARL 45

RESULT 13
 ID O97152 PRELIMINARY; PRT; 52 AA.
 AC O97152;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN Name=pol;
 OS Drosophila arizonae (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tovar F.J., Rodarte S.R., Almeida R.C., Leoncini O.,
 RL Submitted (DDB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF114256; AA018018.1; -;
 DR FlyBase; FBgn0043769; Dair\RI-element\pol.
 KW GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 RN RNA-directed DNA polymerase.
 FT NON_TER 1
 FT 52
 SQ SEQUENCE 52 AA; 6215 MW; B511A4FC41B2A40A CRC64;

Query Match 100.0%; Score 21; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 26 HARL 29

RESULT 14
 ID Q6GVJ3 PRELIMINARY; PRT; 52 AA.
 AC Q6GVJ3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycosyltransferase (Fragment).
 GN Name=wbcf;
 OS Burkholderia cenocepacia.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=95486;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K56-2;

RA Ortega X., Hunt T.A., Valvano M.A.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY633623; AAT48330.1; -;
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1
 FT 1
 SQ SEQUENCE 52 AA; 5931 MW; 837076987AD49A80 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 16 HARL 19

RESULT 15
 ID Q8XUV9 PRELIMINARY; PRT; 57 AA.
 AC Q8XUV9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein Rsc3074.
 GN Name=RS00523; OrderedLocNames=RSC3074;
 OS Ralstonia solanacearum (Pseudomonas solanacearum),
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choigne N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Sagnier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RL "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502 (2002).
 DR EMBL; AL646073; CAD16783.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 57 AA; 6465 MW; 034B74E8142BEDD2 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 39 HARL 42

RESULT 16
 ID O27782 PRELIMINARY; PRT; 59 AA.
 AC O27782;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein MTH1750.
 GN OrderedLocNames=MTH1750;
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiواني N., Caruso A., Bueh D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deitah: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AEO00930; AAB86220.1; -;
 DR PIR; B69101; B69101.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 59 AA; 6658 MW; 6559DBB37EED72F0 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 59;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 15 HARL 18

RESULT 17

Q8NWM0 Q8NWM0 PRELIMINARY; PRT; 61 AA.
 AC Q8NWM0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein MW1377.
 GN OrderedLocustNames=MW1377;
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004827; BAB95242.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 61 AA; 6923 MW; 632P2454DA3C0422 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 9 HARL 12

RESULT 18

Q69SF4 Q69SF4 PRELIMINARY; PRT; 62 AA.
 AC Q69SF4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSJNBa0008C11.4 (Hypothetical protein
 DE OJ1136 A05.30).
 GN Name=OSJNBa0008C11.4; Synonyms=OJ1136 A05.30;
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
 RT clone:OSJNBa0008C11.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
 RT clone:OJ1136 A05.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005098; BAD30814.1; -;
 DR EMBL; AP003748; BAD30181.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 62 AA; 6485 MW; B1A8DAAE1372BA02 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 28 HARL 31

RESULT 19

Q7XZX7 Q7XZX7 PRELIMINARY; PRT; 64 AA.
 AC Q7XZX7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein OSUNBa0093M23.1.
 GN Name=OSUNBa0093M23.1;
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC138001; AAP68416.1; -;
 DR Gramene; Q7XZX7; -;
 KW Hypothetical protein.
 SQ SEQUENCE 64 AA; 6992 MW; AB88D861DB423B99 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 22 HARL 25

RESULT 20

Q07026 Q07026 PRELIMINARY; PRT; 65 AA.
 ID Q07026;
 AC Q07026;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE RfbQ protein.
GN Name=rfbQ;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=017;
RX MEDLINE=92212870; PubMed=1372980;
RA Stroehner U.H., Karageorgos L.E., Morona R.; Manning P.A.;
RT "Serotype conversion in *Vibrio cholerae* O1";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2566-2570(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=017;
RX MEDLINE=95309704; PubMed=7540582; DOI=10.1016/0378-1119(95)00124-0;
RA Manning P.A., Stroehner U.H., Karageorgos L.E., Morona R.;
RT "Putative O-antigen transport genes within the rfb region of *Vibrio*
RL cholerae O1 are homologous to those for capsule transport.";
RX Gene 158:1-7(1995).
DR EMBL: X59554; CAA42147.1; -;
DR PIR: S28481; S28481.1;
SQ SEQUENCE 65 AA; 7577 MW; 59FA6094E686B544 CRC64;
Query Match 100.0%; Score 21; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
DB 53 HARL 56
RESULT 21
Q63JY7
ID Q63JY7 PRELIMINARY; PRT; 66 AA.
AC Q63JY7
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BPSS1578a;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Cresset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabbitts E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilailai S., Stevens K., Tumapa S., Vesaratchaveit M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL: BX571966; CAH39052.1; -;
KW Hypothetical protein.
SQ SEQUENCE 66 AA; 6981 MW; 7701C9906B3366B7 CRC64;
Query Match 100.0%; Score 21; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 53 HARL 53
RESULT 22
Q8UJ23
ID Q8UJ23 PRELIMINARY; PRT; 67 AA.
AC Q8UJ23
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0115.
GN OrderedLocuNames=Atu0115;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
RT C58";
RL Science 294:2317-2323(2001).
DR EMBL: AE008985; AAL41140.1; -;
DR PIR: AF2590; AF2590.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 67 AA; 7608 MW; 351679E2DBE08499 CRC64;
Query Match 100.0%; Score 21; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
DB 53 HARL 56
RESULT 23
Q6MX20
ID Q6MX20 PRELIMINARY; PRT; 67 AA.
AC Q6MX20
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Rv2988a;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekala E., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 DR EMBL; BX842581; CAB55536.1; -.
 DR InterPro; IPR009082; His_kin_homodim.
 KW Complete proteome.
 SQ SEQUENCE 67 AA; 7658 MW; 7E4DC80E86EF73DB CRC64;

Query Match 100.0%; Score 21; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 17 HARL 20

RESULT 24

Q7TXG9 PRELIMINARY; PRT; 67 AA.
 AC Q7TXG9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein Mb3023c.
 GN OrderedLocusNames=Mb3023c;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=AF2122/97;

RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
 RT "The complete genome sequence of Mycobacterium bovis."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 DR EMBL; BX248344; CAD96710.1; -.
 DR InterPro; IPR009082; His_kin_homodim.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 67 AA; 7658 MW; 7E4DC80E86EF73DB CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 17 HARL 20

RESULT 25

Q82PY5 PRELIMINARY; PRT; 68 AA.
 AC Q82PY5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative transcriptional regulator.
 GN OrderedLocusNames=SAV736;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=MA-4680;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 DOI=10.1073/pnas.211433198;

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis."
 RL Nat. Biotechnol. 21:526-531(2003).
 CC -I- SIMILARITY: Contains 1 HTH LYSR-type DNA-binding domain.
 DR EMBL; AF005023; BAC68446.1; -.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR000847; HTH_LYSR.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF00126; HTH_1; 1.
 DR PRINTS; PR00039; HTHLYSR.

DR PROSITE; PS50931; HTH_LYSR; 1.
 KW Complete proteome; DNA-binding; Transcription;
 KW Transcription regulation.

SQ SEQUENCE 68 AA; 8163 MW; 19297FED6CD96F47 CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 46 HARL 49

RESULT 26

Q8VAB5 PRELIMINARY; PRT; 68 AA.
 AC Q8VAB5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Wav511 (WSSV037).
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
 OX NCBI_TaxID=92652;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21548311; PubMed=11689662;
 RX DOI=10.1128/JVI.75.23.11811-11820.2001;

RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RT "Complete genome sequence of the shrimp white spot bacilliform
 RT virus."
 RL J. Virol. 75:11811-11820(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;

RA Tsai M.F., Yu H.T., Tzeng H.P., Leu J.H., Chou C.M., Huang C.J.,
 RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
 RT "Identification and characterization of a shrimp white spot syndrome
 RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
 RT cellular-type thymidine kinase and thymidylate kinase."
 RL Virology 277:100-110(2000).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;

RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
 RA Lo C.F., Kou G.H.;
 RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
 RT spot syndrome virus and characterization of the motif important for
 RT targeting VP35 to the nuclei of transfected insect cells.";

```

RL Virology 293:44-53 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Lo C.-F., Kou G.-H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332093; AAL33512.1; -
DR EMBL; AF440570; AAL88905.1; -
SQ SEQUENCE 68 AA; 8104 MW; 61908A8049D134D CRC64;

Query Match 100.0%; Score 21; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 24 HARL 27

RESULT 27
Q943U1 PRELIMINARY; PRT; 70 AA.
ID AC Q943U1;
DC 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B157F09.18 protein (P0025H06.4 protein).
GN Names=B157F09.18; Synonyms=P0025H06.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoch Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316 (2002).
DR EMBL; AP003207; BAB64092.1; -
DR EMBL; AP003312; BAC10717.1; -
DR Gramene; Q943U1; -
SQ SEQUENCE 70 AA; 8053 MW; 1038D3DE5DEF6AFD CRC64;

Query Match 100.0%; Score 21; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 45 HARL 48

RESULT 28
Y698 ARCFU STANDARD; PRT; 71 AA.
ID AC Q29560;
DC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein AF0698.

OrderedLocusNames=AF0698;
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OX NCBI_TaxID=2234;
RN RP SEQUENCE FROM N.A.
RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham M.D., Kyrpides N.C.,
RA Fleischmann D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Uterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370 (1997).

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EMBL; AE001056; AAB90546.1; -
DR PIR; B69337; B69337.
DR TIGR; AF0698; -
SQ SEQUENCE 71 AA; 8002 MW; 803C030788157824 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 4 HARL 7

RESULT 29
Q740G1 PRELIMINARY; PRT; 71 AA.
ID AC Q740G1;
DC 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP1390;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN RP SEQUENCE FROM N.A.
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; AAS03707.1; -
DR InterPro; IPR005651; DUF343.
DR Pfam; PF03966; DUF343.1.
KW Complete proteome.
SQ SEQUENCE 71 AA; 8107 MW; 6160BE8E88B7D768 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 58 HARL 61

RESULT 30

Q8G1M5 ID Q8G1M5 PRELIMINARY; PRT; 72 AA.
 AC Q8G1M5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=BR0688;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.P.,
 RA Read T.D., Dodson R.J., Unayam L.A., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
 RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
 RA Fraser C.M.;
 RT "the Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014375; AAN29617.1; -.
 DR TIGR; BR0688; -.
 KW Complete proteome.
 SQ SEQUENCE 72 AA; 7854 MW; C7075427DA31EAB5 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 72;

Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 68 HARL 71

RESULT 31

Q6Z3U0 ID Q6Z3U0 PRELIMINARY; PRT; 73 AA.
 AC Q6Z3U0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNBa0025J22.12 (Hypothetical protein
 DE QJ1134 H03.22).
 GN Name=OSJNBa0025J22.12; Synonyms=OJ1134_H03.22;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005245; BAD10172.1; -.
 DR EMBL; AP003883; BAD08835.1; -.

KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 7735 MW; BBF27A50CC74B3E9 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 73;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 31 HARL 34

RESULT 32

Q7UH15 ID Q7UH15 PRELIMINARY; PRT; 73 AA.
 AC Q7UH15;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=RB4902;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294141; CAD78164.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 73 AA; 8367 MW; A49CF28278CD1F01 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 73;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 36 HARL 39

RESULT 33

Q89BQ6 ID Q89BQ6 PRELIMINARY; PRT; 73 AA.
 AC Q89BQ6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bsl8092 protein.
 GN OrderedLocuNames=bsl8092;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Teurouka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005964; BAC53357.1; -.

KW Complete proteome. 7881 MW; D79C3A6D35D5E7 CRC64;
SQ SEQUENCE 73 AA; 7881 MW; D79C3A6D35D5E7 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 66 HARL 69

RESULT 34

Q6WL03 PRELIMINARY; PRT; 74 AA.
AC Q6WL03;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GATA binding protein 2 (Fragment).
GN Name=GATA2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14970692; DOI=10.1159/000075738;
RA Van Poucke M., Verle M., Chardon P., Jacobs K., Genet C.,
RA Mattheeuws M., Van Zeveren A., Peelman L.J.;
RT "A refined comparative map between porcine chromosome 13 and human
RT chromosome 3";
RL Cytogenet. Genome Res. 102:133-138(2003).
DR EMBL: AY280857; AAO16313.1; --
FT NON_TER 1 74
FT TER 74 74
SQ SEQUENCE 74 AA; 7931 MW; 7808EEF5B9E3B691 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 24 HARL 27

RESULT 35

Q84YV8 PRELIMINARY; PRT; 74 AA.
AC Q84YV8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein OSJNBa0077B15.139.
GN Name=OSJNBa0077B15.139;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=33947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
RT clone:OSJNBa0077B15.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005473; BACS7359.1; --
DR Gramene; Q84YV8; --
DR Hypothetical protein.
KW SEQUENCE 74 AA; 8278 MW; 2116CD24AFD5ADF3 CRC64;
Query Match 100.0%; Score 21; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 39 HARL 42

RESULT 36

O33186 PRELIMINARY; PRT; 74 AA.
AC O33186; Q7D855;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocName=MT1724, Rv1684;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekaita F., Badcock K., Baaham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagers K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL: BX842577; CAB10941.1; --
DR EMBL: AE000516; AAX45992.1; --
DR PIR: C70501; C70501.
DR TIGR: MT1724; --
DR TubercuList; Rv1684; --
DR InterPro: IPR005651; DUF343.
DR Pfam: PF03966; DUF343.1
SQ SEQUENCE 74 AA; 8289 MW; 84784E241903C263 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 61 HARL 64

RESULT 37

Q7TZS8 PRELIMINARY; PRT; 74 AA.
AC Q7TZS8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Mbl1710A.
GN Name=Mbl1710A; ORFNames=Mbl1710A;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RA MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duhoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Akkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248339; CAD96378.1; -.
DR InterPro; IPR005651; DJF343.
DR Complete proteome.
DR Pfam; PF03966; DUF343; 1.
KW Complete proteome.
SQ SEQUENCE 74 AA; 8289 MW; 84784E241903C263 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 61 HARL 64

RESULT 38
Q9IK63 PRELIMINARY; PRT; 74 AA.
ID Q9IK63
AC Q9IK63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20216631; PubMed=10751348;
RA Rodriguez-Inigo E., Casqueiro M., Bartolome J., Ortiz-Movilla N.,
RA Lopez-Alcorocho J.M., Herrero M., Manzarbeitia F., Oliva H.,
RA Careno V.;
RT "Detection of TT virus DNA in liver biopsies by in situ hybridization.";
RL Am. J. Pathol. 156:1227-1234(2000).
DR EMBL; AF216403; AAF79086.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 8318 MW; CEE6503663BFD802 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 45 HARL 48

RESULT 39
Q85JV7 PRELIMINARY; PRT; 75 AA.
ID Q85JV7
AC Q85JV7;
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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase 3 (Fragment).
OS Parga condei.
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Tentredinoidea; Pergidae;
OC Parga.
OX NCBI_TaxID=32411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22584006; PubMed=12698290; DOI=10.1007/s00239-002-2420-3;
RA Dowton M., Castro L.R., Campbell S.L., Bargon S.D., Austin A.D.;
RT "Frequent mitochondrial gene rearrangements at the Hymenopteran nad3-
nad5 junction.";
RL J. Mol. Evol. 56:517-526(2003).
CC -I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -I- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AF489462; AAO49080.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4; 1.
DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8957 MW; B2BE0CB347B99CF CRC64;

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 6 HARL 9

RESULT 40
O65817 PRELIMINARY; PRT; 75 AA.
ID O65817
AC O65817;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chlorophyll a/b-binding protein (Fragment).
GN Names=CP29;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf.
RA Humbeck K., Krupinska K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006296; CAA06961.1; -.
DR PIR; T06193; T06193.
DR GO; GO:0009765; P:photosynthesis light harvesting; IEA.
DR InterPro; IPR001344; Chloro_Abbind.
DR Pfam; PF00504; Chloroa_b_bind; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 7988 MW; 5442D30B9E61057D CRC64;

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 30 HARL 33
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RESULT 41
Q70WA2 PRELIMINARY; PRT; 76 AA.
AC Q70WA2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Recombinase A (Fragment).
GN Name=recA;
OS Acetobacter diazotrophicus (Gluconacetobacter diazotrophicus).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=33396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-type strain: LMG 7603;
RA Marzotto M., Mecchi D., Gastaldelli M., Felis G.E., Torriani S.,
RA Dellaglio F.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of
CC single-stranded DNA, the ATP-dependent uptake of single-stranded
CC DNA by duplex DNA, and the ATP-dependent hybridization of
CC homologous single-stranded DNAs. It interacts with lexA causing
CC its activation and leading to its autocatalytic cleavage (By
CC similarity).
CC -1- SIMILARITY: Belongs to the recA family.
DR EMBL; AJ519485; CA58029.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003684; F:damaged DNA binding; IEA.
DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0009432; P:SOS response; IEA.
DR InterPro; IPR001553; RECA.
DR Pfam; PF00154; RECA; 1.
DR PROSITE; PS00229; RECA_2; 1.
DR PROSITE; PS0162; RECA_1; 1.
KW ATP-binding; DNA damage; DNA recombination; DNA repair; DNA-binding;
KW SOS response.
FT NON_TER 1
FT NON_TER 76
SQ SEQUENCE 76 AA; 8166 MW; EE4957681AFCEDAC CRC64;

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 35 HARL 38
|||||

RESULT 42
Q88YS2 PRELIMINARY; PRT; 78 AA.
AC Q88YS2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prophage Lpl protein 49.
GN OrderedLocuNames=lp_0672;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
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RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RL "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935253; CAD63277.1; -.
KW Complete proteome.
SQ SEQUENCE 78 AA; 9282 MW; 37AC50349E21D87C CRC64;

Query Match 100.0%; Score 21; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 10 HARL 13
|||||

RESULT 43
Q7R3N8 PRELIMINARY; PRT; 79 AA.
AC Q7R3N8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 39 37979 37740.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB0100014; EAA41918.1; -.
SQ SEQUENCE 79 AA; 8637 MW; 7C2196274B218609 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 31 HARL 34
|||||

RESULT 44
Q6KIW8 PRELIMINARY; PRT; 79 AA.
AC Q6KIW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein B1279D09.4 (Hypothetical protein
DE P0523B07.42).
GN Name=B1279D09.4; Synonyms=P0523B07.42;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
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RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
RT Clone.P0523B07.",
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006441; BAD23750.1; -.
DR EMBL; AP005589; BAD23436.1; -.
KW Hypothetical protein.
SQ SEQUENCE 79 AA; 9247 MW; F6AA2D0849598632 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 11 HARL 14

RESULT 45

Q9XB07 Q9XB07 PRELIMINARY; PRT; 79 AA.
AC Q9XB07;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=taB;
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytophacterales; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ER-15;
RX MEDLINE=20055630; PubMed=10589713;
RA Paltan Y., Orr E., Ron E.Z., Rosenberg E.;
RT "Genetic and functional analysis of genes required for the post-
RT modification of the polyketide antibiotic TA of Myxococcus xanthus.";
RL Microbiology 145:3059-3067(1999).
DR EMBL; AJ132503; CAB46501.1; -.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR006163; PspPanteth_bind.
DR PROSITE; PS50075; ACP DOMAIN; 1.
SQ SEQUENCE 79 AA; 8730 MW; 4FF1C5867B8192F7 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 76 HARL 79

RESULT 46

Q89NV1 Q89NV1 PRELIMINARY; PRT; 79 AA.
AC Q89NV1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bsr3733 protein.
GN OrderedLocusNames=bsr3733;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA1110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,

RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005948; BAC48998.1; -.
KW Complete proteome.
SQ SEQUENCE 79 AA; 9132 MW; CFE036408F0CEAF8 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 52 HARL 55

RESULT 47

Q841N1 Q841N1 PRELIMINARY; PRT; 80 AA.
AC Q841N1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VacB (Fragment).
GN Name=vacB;
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GC41;
RX PubMed=12675793;
RA Conover G.M., Derre I., Vogel J.P., Isberg R.R.;
RT "The Legionella pneumophila Lida protein: a translocated substrate of
RT the Dot/Icm system associated with maintenance of bacterial
RT integrity.";
RL Mol. Microbiol. 48:305-321(2003).
DR EMBL; AV178780; AAO61479.1; -.
DR GO; GO:0004540; F:ribonuclease activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR001900; Ribonuclease_II.
DR Pfam; PF00773; RNB; 1.
FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 9406 MW; A746DBD29D6E0DC2 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 35 HARL 38

RESULT 48

Q8XVY7 Q8XVY7 PRELIMINARY; PRT; 80 AA.
AC Q8XVY7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PROBABLE TRANSMEMBRANE PROTEIN.
GN Name=RS00033; OrderedLocusNames=RSC2688;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.


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RC STRAIN-CM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Manganot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choïene N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigrier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646071; C:integral to membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR KW Complete proteome; Transmembrane.
SQ SEQUENCE 80 AA; 8473 MW; DD63737FD6B0CB69 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 46 HARL 49

RESULT 49
ID Q9PDG2 PRELIMINARY; PRT; 80 AA.
AC Q9PDG2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf1417;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OC NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003972; AA984226.1; -.
DR FIK; F82684; F82684.
DR KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 80 AA; 8778 MW; 9376F5FBA2D96C7D CRC64;

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Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 53 HARL 56

RESULT 50
ID Q9M675 PRELIMINARY; PRT; 81 AA.
AC Q9M675;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Cystathionine-gamma synthase (Fragment).
OS Cucumis melo (Muskmelon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids I; Cucurbitales; Cucurbitaceae; Cucumis.
OC NCBI_TaxID=3656;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20177879; PubMed=10712562; DOI=10.1104/pp.122.3.977;
RA Hadfield K.A., Dang T., Guis M., Pech J.-C., Bouzayen M.,
RA Bennett A.B.;
RT "Characterization of ripening-regulated cDNAs and their expression in
RT ethylene-suppressed charantais melon fruit.";
RL Plant Physiol. 122:977-983(2000).
DR EMBL; AF206626; AAF64422.1; -.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 8883 MW; 5B043AA22FD8D247 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 6 HARL 9

RESULT 51
ID Q67W97 PRELIMINARY; PRT; 82 AA.
AC Q67W97;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0460H04.9 (Hypothetical protein
DE P0709F06.30).
GN Names=P0460H04.9; Synonyms=P0709F06.30;
OC Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0460H04.9";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0709F06.30";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003712; BAD37572.1; -.

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DR EMBL: AP003579; BAD37555.1; -
KW Hypothetical protein.
SQ SEQUENCE 82 AA; 9606 MW; E099FE334E3DDCA6 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 9 HARL 12

RESULT 52
ID Q711A9 PRELIMINARY; PRT; 82 AA.
AC Q711A9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Sucrose-6-phosphate hydrolase (EC 3.2.1.26) (Fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OC NCBI_TaxID=23397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4797;
RA Langenheim J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
DR EMBL: AF496346; AAQ07028.1; -
DR GO: GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR001362; Glyco hydro_32.
DR Pfam: PF00251; Glyco hydro_32_1.
DR Glycosidase; Hydrolase.
FT NON TER 1
FT NON TER 82
FT NON TER 82
SQ SEQUENCE 82 AA; 8862 MW; 19142D798ED208DA CRC64;

Query Match 100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 31 HARL 34

RESULT 53
ID Q821B6 PRELIMINARY; PRT; 82 AA.
AC Q821B6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Citrate lyase acyl carrier protein (Gamma chain).
GN Name=citD; OrderedLocusNames=SF0534;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OC NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RA MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;

RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441 (2002).
DR EMBL: AE015084; AAN42178.1; -
DR GO: GO:0016829; F:lyase activity; IEA.
DR InterPro: IPR006495; CitD.
DR Pfam: PF04953; CitD; 1.
DR ProDom: PD015389; CitD; 1.
DR TIGRFAMs: TIGR01608; citD; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 82 AA; 9089 MW; B92FC0C6A927808C CRC64;

Query Match 100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 60 HARL 63

RESULT 54
CI16 HUMAN STANDARD; PRT; 83 AA.
ID CI16 HUMAN STANDARD; PRT; 83 AA.
AC Q9BUW7; Q9Y3F7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical UPF0184 protein C9orf16 (EST00098).
GN Names=C9orf16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Srapletenko M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE OF 27-83 FROM N.A.
RX MEDLINE=99299247; PubMed=10369878; DOI=10.1093/hmg/8.7.1313;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT evolution and the cloning of disease genes.";
RN Hum. Mol. Genet. 8:1313-1320 (1999).
CC -1- SIMILARITY: Belongs to the UPF0184 (EST00098) family.
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EMBL; BC001857; AA01857.1; -
 EMBL; BC008887; AA08887.1; -
 EMBL; Y17450; CAB44344.1; -
 Genew; HGNC:17823; C9orf16.
 InterPro; IPR005374; UPF0184.
 Pfam; PF03670; UPF0184; 1.
 ProDom; PD479232; UPF0184; 1.
 Coiled coil; Hypothetical protein.
 Coiled coil (Potential).
 L -> V (in Ref. 2).
 DOMAIN 25 74
 CONFLICT 35 35
 SEQUENCE 83 AA; 9054 MW; EBEID0AFAAD6DABB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 83;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 53 HARL 56

RESULT 55
 ID C116 MOUSE STANDARD; PRT; 83 AA.
 AC P58686;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Hypothetical UPF0184 protein C9orf16 homolog.
 GN Name=C9orf16;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nkaido I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirral L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brucic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Perlee G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlesch C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Watanabe A.,
 RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayaishizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SIMILARITY: Belongs to the UPF0184 (EST00098) family.
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EMBL; AK003598; -; NOT ANNOTATED_CDS.
 EMBL; BC024615; AAH24615.1; -
 EMBL; BC049639; AAH49639.1; -
 MGD; MGI:1920987; 1110008P14Rik.
 DR InterPro; IPR005374; UPF0184.
 DR Pfam; PF03670; UPF0184; 1.
 DR ProDom; PD479232; UPF0184; 1.
 DR Coiled coil; Hypothetical protein.
 DR DOMAIN 25 74 Coiled coil (Potential).
 FT SEQUENCE 83 AA; 9055 MW; 4D6D5BA98B7D36D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 83;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 53 HARL 56

RESULT 56
 ID Q9K5X7 PRELIMINARY; PRT; 83 AA.
 AC Q9K5X7;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE BH3959 protein.
 DE OrderedLocusNames=BH3959;
 GN Bacillus halodurans.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeki N.,
 RA Fuji F., Hiram C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 85 AA; 9321 MW; F384B3E113DF876 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 85;

Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 39 HARL 42

RESULT 60

Q8UIC1 PRELIMINARY; PRT; 85 AA.

AC Q8UIC1; OTD1K7;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Hypothetical protein Atu0376 (AGR C.659p).

GN OrderedLocustNames=AGR_C_659; Atu0376;

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

OX NCBI_TaxID=176299;

[1]

SEQUENCE FROM N.A.

STRAIN=Dupont;

RA MEDLINE=1608550; PubMed=11743193; DOI=10.1126/science.1066804;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

RA Raymond C., Rouse G., Saenphumachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Neester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

CS8.";

Science 294:2317-2323(2001).

[2]

SEQUENCE FROM N.A.

STRAIN=Cereon;

RA MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,

RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens CS8.";

Science 294:2323-2328(2001).

RA EMBL; AE009008; AAL41398.1;

RA EMBL; AE007975; AAK86193.1;

RA PIR; AH2622; AH2622.

RA PIR; H97404; H97404.

RA InterPro; IPR009531; DUF1150.

RA Pfam; PF06620; DUF1150; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 85 AA; 9466 MW; 51BB33B66A33219 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 85;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 7 HARL 10

RESULT 61

Q66074

ID Q66074 PRELIMINARY; PRT; 85 AA.

AC Q66074;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Virion protein (Fragment).

OS Canine herpesvirus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae.

OX NCBI_TaxID=37110;

[1]

SEQUENCE FROM N.A.

RA MEDLINE=96145133; PubMed=8558127;

RA Remond M., Sheldrick P., Lebreton P., Nardeux P., Foulon T.;

RT "Gene organization in the UL region and inverted repeats of the canine

herpesvirus genome.";

J. Gen. Virol. 77:37-48(1996).

RL EMBL; X90444; CAA62069.1;

DR GO; GO:0006323; P:DNA packaging; IEA.

DR InterPro; IPR002660; Herpes_UL6.

DR Pfam; PF01763; Herpes_UL6; 1.

DR ProDom; PD003210; Herpes_UL6; 1.

FT NON_TER 1

FT NON_TER 85

SQ SEQUENCE 85 AA; 9584 MW; 3DF46D8AAE18ADCF CRC64;

Query Match 100.0%; Score 21; DB 2; Length 85;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 30 HARL 33

RESULT 62

Q649W2

ID Q649W2 PRELIMINARY; PRT; 86 AA.

AC Q649W2;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein.

GN ORFNames=G234A6_26;

OS uncultured archaeon Gzfos34A6.

OC Archaea; environmental samples.

OX NCBI_TaxID=285405;

[1]

SEQUENCE FROM N.A.

RA PubMed=15353801;

RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,

RA Richardson P.M., DeLong E.F.;

RT "Reverse methanogenesis: testing the hypothesis with environmental

genomics.";

Science 305:1457-1462(2004).

RL Science 305:1457-1462(2004).

[2]

SEQUENCE FROM N.A.

RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;

RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY714859; AAU83815.1;

KW Hypothetical protein.

SQ SEQUENCE 86 AA; 10255 MW; DB87CC9FB2ACD8C1 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|
|
|
|
Db 21 HARL 24

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RESULT 63
Q9FD17 PRELIMINARY; PRT; 87 AA.
AC Q9FD17; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acyl carrier protein.
GN Name=rubC;
OS Streptomyces collinus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=42684;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=DSM2012;
RA Saito H., Bruenker P., Martin R., Minas W.
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of the protein (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
DR EMBL; AF293355; AAG03069.1; -.
DR HSSP; Q02054; 2AF8.
DR GO; GO:0000036; F:acyl carrier activity; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR003231; Acyl carrier.
DR InterPro; IPR006163; Phosphanteth_bind.
DR InterPro; IPR006162; Pantne_S.
DR Pfam; PF00550; PP-binding; 1.
DR ProDom; PD000887; Acyl carrier; 1.
DR PROSITE; PS00075; ACP DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW Phosphopantetheine.
SQ SEQUENCE 87 AA; 9792 MW; 235B0DCC875F14C0 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 79 HARL 82

RESULT 64
Q8PDJ9 PRELIMINARY; PRT; 87 AA.
AC Q8PDJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Xanthomonadin biosynthesis related protein 1.
GN Name=plgH; OrderedLocusNames=XCC0337;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=3340;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RA MEDLINE=2202145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cimarotte G., Cavanaugh F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

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RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AB012130; AAM39656.1; -.
KW Complete proteome.
SQ SEQUENCE 87 AA; 9068 MW; 4A7DB3FE7DAD0F6E CRC64;

Query Match 100.0%; Score 21; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 68 HARL 71

RESULT 65
Q9FBZ3 PRELIMINARY; PRT; 87 AA.
AC Q9FBZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO7189.
GN ORFNames=SC8A11.17c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939130; CAC01589.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 87 AA; 9955 MW; F0008D1049B11D4B CRC64;

Query Match 100.0%; Score 21; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
Db 41 HARL 44

RESULT 66
Q9YKD5 PRELIMINARY; PRT; 88 AA.
AC Q9YKD5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Precocot protein.
OS Tomato yellow leaf curl virus - Israel.

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OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN NCBI_TaxID=66366;
 RX SEQUENCE FROM N.A.
 RA Peterschmitt M., Granier M., Aboulama S.;
 RT "First report of tomato yellow leaf curl Geminivirus virus in
 RL Morocco."; 83:1074-1074(1999).
 DR Plant Dis.
 DR EMBL; AJ133491; CAB38575.1; -
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR002511; Geminivir_V1.
 DR Pfam; PF01524; Geminivir_V1; 1.
 DR ProDom; PD002978; Geminivir_V1; 1.
 KW Coat protein.
 SQ SEQUENCE 88 AA; 10378 MW; 32D149F7EB0F9C39 CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. NO. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 65 HARL 68
 RESULT 67
 Q73SS2 PRELIMINARY; PRT; 89 AA.
 AC Q73SS2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP4001;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017241; AAS06551.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 89 AA; 9817 MW; B21FA3E5F31E7C4D CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 89;
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 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 25 HARL 28
 RESULT 68
 Q7P1L8 PRELIMINARY; PRT; 89 AA.
 AC Q7P1L8;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=CV0195;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;

RX MEDLINE=22892880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Baptista A.J., de Araujo M.P.F.,
 RA Aetoli-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Buritty H.A.,
 RA Camargo A.A., Cardoso D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinati F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.T., Franco G.R., Freitas N.S.A., Fulan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 DR EMBL; AE016910; AAO57874.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 89 AA; 10224 MW; EB0C6F88429AAD9 CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. NO. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 78 HARL 81
 RESULT 69
 Q7TM11 PRELIMINARY; PRT; 89 AA.
 AC Q7TM11;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative xylanase (fragment).
 OS uncultured organism.
 OC unclassified; environmental samples.
 OX NCBI_TaxID=155900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Radomski C.C.A., Seow K.T., Warren R.A.J., Yap W.H.;
 RT "Method for isolating xylanase gene sequences from soil DNA,
 RT compositions useful in such method and compositions obtained
 RT thereby";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chatteranjan S., Radomski C.C., Chow M.L., Davies J., Axelrod P.E.;
 RT "Retrieval of novel DNA sequences encoding xylanase-like genes from
 RT British Columbia forest soils";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF427422; AAP87520.1; -
 DR HSP; P07986; 1EXP.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase; Xylan degradation.
 FT NON_TER 1 1
 FT TER 89 89

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SQ SEQUENCE 89 AA; 10346 MW; 5983DD37183C210F CRC64;
Query Match 100.0%; Score 21; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
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Db 73 HARL 76

RESULT 70
Q93SB6 ID Q93SB6 PRELIMINARY; PRT; 92 AA.
AC Q93SB6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Frankia sp. Ar13.
OG Plasmid pFQ31.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Frankiaceae; Frankia.
ON NCBI_TaxID=1858;
RX SEQUENCE FROM N.A.
RP STRAIN=Ar13;
RX MEDLINE=21184415; PubMed=11287155;
RA Lavire C., Louis D., Perriere G., Briolay J., Normand P.,
RA Cournoyer B.;
RT "Analysis of pFQ31, a 8551-bp cryptic plasmid from the symbiotic
RT nitrogen-fixing actinomycete Frankia."
RL FEMS Microbiol. Lett. 197;111-116 (2001).
DR EMBL; AJ297945; CAC39346.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 92 AA; 10054 MW; B6A0D4F13CF6FED8 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
    ||||
Db 24 HARL 27

RESULT 71
VP44 ID VP44 BPAPS STANDARD; PRT; 93 AA.
AC Q91Q4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative protein P44.
GN Name=44;
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
ON NCBI_TaxID=106199;
RX SEQUENCE FROM N.A.
RX MEDLINE=9420383; PubMed=10489345; DOI=10.1006/viro.1999.9902;
RA van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RT the secondary endosymbiont of acyrthosiphon pisum."
RL Virology 262;104-113 (1999).
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CC or send an email to license@isb-sib.ch).
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CC EMBL; AF157835; AAF03987.1; -.
DR Hypothetical protein.
KW SEQUENCE 93 AA; 10356 MW; B7EBE57CB8BB3C63 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 93;
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QY 1 HARL 4
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Db 67 HARL 70

RESULT 72
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AC Q18842;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein C54G10.1.
DE ORFNames=C54G10.1;
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RX SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Matthews L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z75532; CAA99809.1; -.
DR PIR; T20227; T20227.
DR WormBase; WBGene0008319; C54G10.1.
DR WormPep; C54G10.1; CE05516.
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10885 MW; C00F5DC151DE15B CRC64;

Query Match 100.0%; Score 21; DB 2; Length 93;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
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Db 19 HARL 22

RESULT 73
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AC Q91113;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PA2292;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RX SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
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RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter D.H., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.N., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL; AE004655; AAG05680.1; -;
 DR PIR; E83358; E83358;
 DR InterPro; IPR010376; DUF971.
 DR Pfam; PF06155; DUF971; 1.
 DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 93 AA; 10732 MW; A38541EC2F12AF22 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 93;
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Qy 1 HARL 4
 Db 31 HARL 34

RESULT 74

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 AC Q88UQ7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Prophage Lp2 protein 47.
 GN OrderedLocustNames=lp_2410;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
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 RN SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of *Lactobacillus plantarum* WCFS1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL; AL935259; CAB64718.1; -;
 KW Complete proteome.
 SQ SEQUENCE 94 AA; 10941 MW; D7AA030959373E55 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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Qy 1 HARL 4
 Db 26 HARL 29

RESULT 75

P83814 PRELIMINARY; PRT; 95 AA.
 AC P83814;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative Nucleotidyltransferase.
 OS *Thermus thermophilus*.

OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP STRUCTURE BY NMR.
 RA Suzuki S., Hatanaka H., Hondoh T., Okumura A., Kuroda Y.,
 RA Kuramitsu S., Shibata T., Inoue Y., Yokoyama S.;
 RL Submitted (NOV-2002) to the PDB data bank.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
 DR InterPro; IPR001201; PAP_25A_core.
 KW 3D-structure.
 SQ SEQUENCE 95 AA; 10582 MW; F8B4497E00977B7E CRC64;

Query Match 100.0%; Score 21; DB 2; Length 95;
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 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 57 HARL 60

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 Job time : 173 secs

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Perfect score: 21

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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2_6/ptodata/1/aa/backfiles1.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	15	3	US-09-347-504-66	Sequence 66, Appl
2	21	100.0	15	4	US-10-161-499-66	Sequence 66, Appl
3	21	100.0	17	1	US-08-399-646-8	Sequence 8, Appl
4	21	100.0	17	1	US-08-607-321-8	Sequence 8, Appl
5	21	100.0	17	2	US-08-963-240-8	Sequence 8, Appl
6	21	100.0	17	2	US-08-605-501-8	Sequence 8, Appl
7	21	100.0	25	4	US-09-270-767-59361	Sequence 58361, A
8	21	100.0	31	4	US-09-403-752A-108	Sequence 108, App
9	21	100.0	31	4	US-09-551-151A-108	Sequence 108, App
10	21	100.0	51	2	US-08-870-518-23	Sequence 23, Appl
11	21	100.0	52	4	US-09-621-976-4733	Sequence 4733, Ap
12	21	100.0	53	1	US-08-228-616-6	Sequence 6, Appl
13	21	100.0	53	3	US-08-446-648-6	Sequence 6, Appl
14	21	100.0	53	4	US-09-982-610-6	Sequence 6, Appl
15	21	100.0	53	5	PCT-US95-04228-6	Sequence 6, Appl
16	21	100.0	55	4	US-09-621-976-4185	Sequence 4185, Ap
17	21	100.0	55	4	US-09-621-976-6961	Sequence 6961, Ap
18	21	100.0	55	4	US-09-513-998C-7554	Sequence 7554, Ap
19	21	100.0	62	4	US-09-621-976-6943	Sequence 6943, Ap
20	21	100.0	63	4	US-09-134-000C-6561	Sequence 6561, Ap
21	21	100.0	63	4	US-09-621-976-5664	Sequence 5664, Ap
22	21	100.0	66	4	US-09-489-039A-11065	Sequence 11065, A
23	21	100.0	66	4	US-09-621-976-4233	Sequence 4233, Ap
24	21	100.0	67	4	US-09-640-211A-2311	Sequence 2311, Ap
25	21	100.0	72	4	US-09-513-999C-7516	Sequence 7516, Ap
26	21	100.0	74	4	US-09-248-736A-28060	Sequence 28060, A
27	21	100.0	77	4	US-09-621-976-6140	Sequence 6140, Ap

ALIGNMENTS

RESULT 1

US-09-347-504-66
; Sequence 66, Application US/09347504
; Patent No. 639075
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT FILING DATE: 1999-07-02
; CURRENT APPLICATION NUMBER: US/09/347,504
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M36A
US-09-347-504-66

Query Match 100.0%; Score 21; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
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Db 3 HARL 6

RESULT 2

US-10-161-499-66
; Sequence 66, Application US/10161499
; Patent No. 6673354
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M36A
US-10-161-499-66

Query Match 100.0%; Score 21; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 3 HARL 6

RESULT 3

US-08-399-646-8
; Sequence 8, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; FILE REFERENCE: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,646
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-399-646-8

Query Match 100.0%; Score 21; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 11 HARL 14

RESULT 4

US-08-607-321-8
; Sequence 8, Application US/08607321
; Patent No. 5716813
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; FILE REFERENCE: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,646
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-399-646-8

Query Match 100.0%; Score 21; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 3 HARL 6

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,321
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-607-321-8

Query Match 100.0%; Score 21; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 11 HARL 14

RESULT 5
US-08-961-240-8
; Sequence 8, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,240

; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-240-8

Query Match 100.0%; Score 21; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 11 HARL 14

RESULT 6
US-08-605-501-8
; Sequence 8, Application US/08605501
; Patent No. 5834287
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,501
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ROBOTA=5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-605-501-8

Query Match 100.0%; Score 21; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
DB 11 HARL 14

RESULT 7

US-09-270-767-58361
Sequence 58361, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58361
LENGTH: 25
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-58361

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
DB 12 HARL 15

RESULT 8

US-09-403-752A-108
Sequence 108, Application US/09403752A
Patent No. 6593132
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
FILE REFERENCE: 10447-005
CURRENT APPLICATION NUMBER: US/09/403,752A
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: U.S. 60/045,148
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: U.S. 60/063,715
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 108
LENGTH: 31
TYPE: PRT
ORGANISM: Mutant preporicrin linker region for MMP-11, PAP-284

US-09-403-752A-108

Query Match 100.0%; Score 21; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
DB 20 HARL 23

RESULT 9

US-09-551-151A-108
Sequence 108, Application US/09551151A
Patent No. 6803358
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-011
CURRENT APPLICATION NUMBER: US/09/551,151A
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 108
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mutant preporicrin linker region for MMP-11, PAP-284
US-09-551-151A-108

Query Match 100.0%; Score 21; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
|||
DB 20 HARL 23

RESULT 10

US-08-870-518-23
Sequence 23, Application US/08870518
Patent No. 5925566
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,518
FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.

; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-870-518-23

Query Match 100.0%; Score 21; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 48 HARL 51

RESULT 11

US-09-621-976-4733
; Sequence 4733, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.Pm
; SEQ ID NO 4733
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4733

Query Match 100.0%; Score 21; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 28 HARL 31

RESULT 12

US-08-222-616-6
; Sequence 6, Application US/08222616
; Patent No. 5635177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,616
; FILING DATE: 4-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/826935
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 821P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-222-616-6

Query Match 100.0%; Score 21; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 41 HARL 44

RESULT 13

US-08-446-648-6
; Sequence 6, Application US/08446648
; Patent No. 6331302
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,648
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-446-648-6

Query Match 100.0%; Score 21; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 41 HARL 44

RESULT 14
US-09-982-610-6
Sequence 6, Application US/09982610
Patent No. 6673343

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
Bennett, Brian D.
Goeddel, David
Lee, James M.
Matthews, William
Tsai, Siao Ping
Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,610

FILING DATE: 17-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,648

FILING DATE: 1996-MAY-23

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0821P3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 53 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-982-610-6

Query Match 100.0%; Score 21; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 41 HARL 44

RESULT 15

PCT-US95-04228-6

Sequence 6, Application PC/TUS9504228

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David

APPLICANT: Lee, James M.

APPLICANT: Matthews, William

APPLICANT: Tsai, Siao Ping

APPLICANT: Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04228

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 53 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-04228-6

Query Match 100.0%; Score 21; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
DB 41 HARL 44

RESULT 16

US-09-621-976-4185

Sequence 4185, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4185
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18...-1.
US-09-621-976-4185

Query Match 100.0%; Score 21; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 32 HARL 35

RESULT 17
US-09-621-976-6961
; Sequence 6961, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6961
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 45
; OTHER INFORMATION: Xaa = Lys,Asn
US-09-621-976-6961

Query Match 100.0%; Score 21; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 28 HARL 31

RESULT 18
US-09-513-999C-7554
; Sequence 7554, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7554
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7554

Query Match 100.0%; Score 21; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 4 HARL 7

RESULT 19
US-09-621-976-6943
; Sequence 6943, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6943
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6943

Query Match 100.0%; Score 21; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 29 HARL 32

RESULT 20
US-09-134-000C-6561
; Sequence 6561, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6561
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6561

Query Match 100.0%; Score 21; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 1 HARL 4

```
Db          44 HARL 47

RESULT 21
US-09-621-976-5664
; Sequence 5664, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5664
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; NAME/KEY: UNSURE
; LOCATION: -18
; OTHER INFORMATION: Xaa = Lys,Gln
; US-09-621-976-5664

Query Match      100.0%; Score 21; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db      46 HARL 49

RESULT 22
US-09-489-039A-11065
; Sequence 11065, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11065
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-11065

Query Match      100.0%; Score 21; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db      25 HARL 28

RESULT 23
US-09-621-976-4233
; Sequence 4233, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

Db          44 HARL 47

RESULT 24
US-09-640-211A-2311
; Sequence 2311, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2311
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-09-640-211A-2311

Query Match      100.0%; Score 21; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db      20 HARL 23

RESULT 25
US-09-513-999C-7516
; Sequence 7516, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
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; SOFTWARE: Patent.pm
; SEQ ID NO 7516
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 63
; OTHER INFORMATION: Xaa= * or Leu or Trp
US-09-513-999C-7516

Query Match      100.0%; Score 21; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      45 HARL 48

RESULT 26
US-09-248-796A-28060
; Sequence 28060, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 28060
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-28060

Query Match      100.0%; Score 21; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      52 HARL 55

RESULT 27
US-09-621-976-6140
; Sequence 6140, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6140
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6140

Query Match      100.0%; Score 21; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      44 HARL 47

RESULT 28
US-09-621-976-6749
; Sequence 6749, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6749
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6749

Query Match      100.0%; Score 21; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      44 HARL 47

RESULT 29
US-09-621-976-6818
; Sequence 6818, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6818
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6818

Query Match      100.0%; Score 21; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      44 HARL 47

RESULT 30
US-09-621-976-6818
; Sequence 6818, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6818
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6818

Query Match      100.0%; Score 21; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      44 HARL 47
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510.646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-28

Query Match 100.0%; Score 21; DB 3; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 46 HARL 49

RESULT 34
US-09-231-818-27
Sequence 27, Application US/09231818
Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231.818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-27

Query Match 100.0%; Score 21; DB 3; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 46 HARL 49

RESULT 35
US-09-635-359B-27
Sequence 27, Application US/09635359B
Patent No. 6670157

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/635,359B

FILING DATE: 09-AUG-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/231,818

FILING DATE: 15-JAN-1999

APPLICATION NUMBER: US 08/403,852

FILING DATE: 10-MAY-1995

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; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-635-359B-27

Query Match      100.0%; Score 21; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      46 HARL 49

RESULT 36
US-09-621-976-6714
; Sequence 6714, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6714
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6714

Query Match      100.0%; Score 21; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      53 HARL 56

RESULT 37
US-09-270-767-43031
; Sequence 43031, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 43031
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43031

Query Match      100.0%; Score 21; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      12 HARL 15

RESULT 38
US-09-107-532A-5045
; Sequence 5045, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5045:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...89
; SEQUENCE DESCRIPTION: SEQ ID NO: 5045:
US-09-107-532A-5045

Query Match      100.0%; Score 21; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      31 HARL 34
```

RESULT 39

US-09-621-976-4499
; Sequence 4499, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4499
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4499

Query Match 100.0%; Score 21; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 44 HARL 47

RESULT 40

US-09-047-125-10
; Sequence 10, Application US/09047125
; Patent No. 5976787
; GENERAL INFORMATION:
; APPLICANT: Leland F. Velicer, Peter Brunovskis,
; TITLE OF INVENTION: Marek's Disease Herpesvirus
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: IBM PS2, Model 50
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: PC-Write 3.02
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/736,335
; FILING DATE: July 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE:
; ORGANISM: herpes simplex virus type 1 (HSV1)
; FEATURE:
; NAME/KEY: peptide of HSV1 gene US10 polypeptide
; LOCATION: 192 TO 282
; OTHER INFORMATION: peptide homologous to the US10 gene
; OTHER INFORMATION: polypeptide of MDV
US-09-047-125-10

Query Match 100.0%; Score 21; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

; ORGANISM: herpes simplex virus type 1 (HSV1)
; FEATURE:
; NAME/KEY: peptide of HSV1 gene US10 polypeptide
; LOCATION: 192 TO 282
; OTHER INFORMATION: peptide homologous to the US10 gene
; OTHER INFORMATION: polypeptide of MDV
US-09-047-125-10

Query Match 100.0%; Score 21; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 30 HARL 33

RESULT 41

US-07-736-335E-10
; Sequence 10, Application US/07736335E
; Patent No. 6087127
; GENERAL INFORMATION:
; APPLICANT: Leland F. Velicer, Peter Brunovskis,
; TITLE OF INVENTION: Marek's Disease Herpesvirus
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: IBM PS2, Model 50
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: PC-Write 3.02
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/736,335E
; FILING DATE: July 25, 1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE:
; ORGANISM: herpes simplex virus type 1 (HSV1)
; FEATURE:
; NAME/KEY: peptide of HSV1 gene US10 polypeptide
; LOCATION: 192 TO 282
; OTHER INFORMATION: peptide homologous to the US10 gene
; OTHER INFORMATION: polypeptide of MDV
US-07-736-335E-10

Query Match 100.0%; Score 21; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

```
Db          30 HARL 33
|||||
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4900
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 45
; OTHER INFORMATION: Xaa=Leu or Pro or Gln or Arg
US-09-513-999C-4900

Query Match      100.0%; Score 21; DB 4; Length 93;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          28 HARL 31

RESULT 45
US-09-502-540-16539
; Sequence 16539, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16539
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-302-540-16539

Query Match      100.0%; Score 21; DB 4; Length 100;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          42 HARL 45

RESULT 46
US-09-621-976-5595
; Sequence 5595, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5595
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1

Db          30 HARL 33
|||||
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4900
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 45
; OTHER INFORMATION: Xaa=Leu or Pro or Gln or Arg
US-09-513-999C-4900

Query Match      100.0%; Score 21; DB 4; Length 93;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          28 HARL 31

RESULT 45
US-09-502-540-16539
; Sequence 16539, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16539
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-302-540-16539

Query Match      100.0%; Score 21; DB 4; Length 100;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          42 HARL 45

RESULT 46
US-09-621-976-5595
; Sequence 5595, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5595
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1

Db          30 HARL 33
|||||
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4900
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 45
; OTHER INFORMATION: Xaa=Leu or Pro or Gln or Arg
US-09-513-999C-4900

Query Match      100.0%; Score 21; DB 4; Length 93;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          28 HARL 31

RESULT 45
US-09-502-540-16539
; Sequence 16539, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16539
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-302-540-16539

Query Match      100.0%; Score 21; DB 4; Length 100;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 HARL 4
|||||
Db          42 HARL 45

RESULT 46
US-09-621-976-5595
; Sequence 5595, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5595
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1
```


; NAME/KEY: UNSURE
; LOCATION: 54
; OTHER INFORMATION: Xaa = Asp,Asn
; NAME/KEY: UNSURE
; LOCATION: -14,50,56
; OTHER INFORMATION: Xaa = Gly,Val
; NAME/KEY: UNSURE
; LOCATION: 33
; OTHER INFORMATION: Xaa = Phe,Ser
US-09-621-976-5595

Query Match 100.0%; Score 21; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 85 HARL 88

RESULT 47
US-09-673-395A-238
; Sequence 238, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKI, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 238
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-238

Query Match 100.0%; Score 21; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 2 HARL 5

RESULT 48
US-09-270-767-57430
; Sequence 57430, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57430
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57430

Query Match 100.0%; Score 21; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 45 HARL 48

RESULT 49
US-09-311-352B-2
; Sequence 2, Application US/09311352B
; Patent No. 6329500
; GENERAL INFORMATION:
; APPLICANT: Webb, Donna J.
; APPLICANT: Gonias, Steven L.
; TITLE OF INVENTION: Transforming Growth Factor-beta Binding Site
; FILE REFERENCE: 00370-02
; CURRENT APPLICATION NUMBER: US/09/311,352B
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-311-352B-2

Query Match 100.0%; Score 21; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 19 HARL 22

RESULT 50
US-09-270-767-34879
; Sequence 34879, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34879
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34879

Query Match 100.0%; Score 21; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 10 HARL 13

RESULT 51
US-09-270-767-50096
; Sequence 50096, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
US-09-270-767-50096

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50096
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50096

Query Match 100.0%; Score 21; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 10 HARL 13

RESULT 52
US-09-328-352-5478
; Sequence 5478, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5478
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5478

Query Match 100.0%; Score 21; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 47 HARL 50

RESULT 53
US-09-266-965-4
; Sequence 4, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 115
; TYPE: PRT

; ORGANISM: Streptomyces anulatus
US-09-266-965-4

Query Match 100.0%; Score 21; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 102 HARL 105

RESULT 54
US-09-949-016-8424
; Sequence 8424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8424
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8424

Query Match 100.0%; Score 21; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 10 HARL 13

RESULT 55
US-09-252-991A-18229
; Sequence 18229, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18229
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18229

Query Match 100.0%; Score 21; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 22 HARL 25
|||||

RESULT 56

US-09-902-540-11756
; Sequence 11756, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,893
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11756
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11756

Query Match 100.0%; Score 21; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 40 HARL 43

RESULT 57

US-09-621-976-4734
; Sequence 4734, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4734
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 25
; OTHER INFORMATION: Xaa = Arg,Thr
US-09-621-976-4734

Query Match 100.0%; Score 21; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 104 HARL 107

RESULT 58

US-08-420-235B-29
; Sequence 29, Application US/08420235B
; Patent No. 5801042
; GENERAL INFORMATION:

APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,235B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 29;
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-420-235B-29

Query Match 100.0%; Score 21; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 100 HARL 103

RESULT 59

US-08-793-624-29
; Sequence 29, Application US/08793624C
; Patent No. 6150093
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 45185-C-PCT-US/JPW
; CURRENT APPLICATION NUMBER: US/08/793,624C
; CURRENT FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-29

Query Match 100.0%; Score 21; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||||
Db 100 HARL 103

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RESULT 60
US-09-902-540-15984
; Sequence 15984, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15984
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15984

Query Match      100.0%; Score 21; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      68 HARL 71

RESULT 61
PCT-US95-10194-29
; Sequence 29, Application PC/TUS9510194
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York
; APPLICANT: City
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10194
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/MSC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-10194-29

Query Match      100.0%; Score 21; DB 5; Length 120;
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      100 HARL 103

RESULT 62
US-09-732-210-663
; Sequence 663, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 663
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-09-732-210-663
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Query Match      100.0%; Score 21; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HARL 4
Db      17 HARL 20
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RESULT 63
US-09-270-767-39085
; Sequence 39085, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39085
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-39085
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Query Match      100.0%; Score 21; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HARL 4
Db      22 HARL 25
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RESULT 64
US-09-270-767-54302
; Sequence 54302, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54302
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-54302

Query Match      100.0%; Score 21; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db      22 HARL 25

RESULT 65
US-09-270-767-40960
; Sequence 40960, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40960
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-40960

Query Match      100.0%; Score 21; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
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Db      102 HARL 105

RESULT 66
US-09-270-767-56176
; Sequence 56176, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56176
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-56176

Query Match      100.0%; Score 21; DB 4; Length 133;
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db      102 HARL 105

RESULT 67
US-09-800-729-194
; Sequence 194, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-800-729-194

Query Match      100.0%; Score 21; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
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Db      60 HARL 63

RESULT 68
US-09-252-991A-18704
; Sequence 18704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18704
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-18704

Query Match      100.0%; Score 21; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
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Db      8 HARL 11

RESULT 69
US-09-270-767-37264
; Sequence 37264, Application US/09270767
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37264
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37264

Query Match      100.0%; Score 21; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
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Db     14 HARL 17

RESULT 70
US-09-270-767-52481
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52481
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52481

Query Match      100.0%; Score 21; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db     14 HARL 17

RESULT 71
US-09-328-352-7201
; Sequence 7201, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7201
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7201

Query Match      100.0%; Score 21; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HARL 4
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Db     89 HARL 92

RESULT 72
US-09-621-976-4315
; Sequence 4315, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4315
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 129
; OTHER INFORMATION: Xaa = Glu,Lys
US-09-621-976-4315

Query Match      100.0%; Score 21; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
      ||||
Db     102 HARL 105

RESULT 73
US-09-540-236-2332
; Sequence 2332, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2332
; LENGTH: 141
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2332

Query Match      100.0%; Score 21; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
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Db     92 HARL 95

RESULT 74
US-09-328-352-4538
; Sequence 4538, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4538
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4538

Query Match 100.0%; Score 21; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 24 HARL 27

RESULT 75
US-09-252-991A-32709
; Sequence 32709, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32709
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32709

Query Match 100.0%; Score 21; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 56 HARL 59

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)

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Listing first 100 summaries

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Published Applications_AA:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	21	100.0	6	14	US-10-146-130-18
5	21	100.0	6	14	US-10-146-130-24
6	21	100.0	6	14	US-10-146-130-31
7	21	100.0	6	14	US-10-146-130-41
8	21	100.0	6	14	US-10-146-130-42
9	21	100.0	7	14	US-10-146-130-19
10	21	100.0	7	14	US-10-146-130-21
11	21	100.0	7	14	US-10-146-130-22
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					Sequence 15, Appl
					Sequence 17, Appl
					Sequence 18, Appl
					Sequence 24, Appl
					Sequence 31, Appl
					Sequence 41, Appl
					Sequence 42, Appl
					Sequence 19, Appl
					Sequence 21, Appl
					Sequence 22, Appl

7	17	US-10-935-254-10	Sequence 10, Appl
8	14	US-10-146-130-40	Sequence 40, Appl
8	16	US-10-657-022-390	Sequence 390, Appl
8	16	US-10-657-022-396	Sequence 396, Appl
8	17	US-10-931-627-15	Sequence 15, Appl
9	16	US-10-657-022-388	Sequence 388, Appl
9	16	US-10-657-022-391	Sequence 391, Appl
9	16	US-10-657-022-393	Sequence 393, Appl
9	16	US-10-657-022-395	Sequence 395, Appl
9	16	US-10-657-022-397	Sequence 397, Appl
9	17	US-10-888-348-32	Sequence 32, Appl
9	17	US-10-888-348-36	Sequence 36, Appl
9	17	US-10-888-348-37	Sequence 37, Appl
9	17	US-10-888-348-41	Sequence 41, Appl
9	17	US-10-888-348-69	Sequence 69, Appl
9	17	US-10-888-348-77	Sequence 77, Appl
9	17	US-10-888-348-84	Sequence 84, Appl
9	17	US-10-888-348-88	Sequence 88, Appl
9	17	US-10-888-348-102	Sequence 102, Appl
9	17	US-10-888-348-153	Sequence 153, Appl
9	17	US-10-888-348-154	Sequence 154, Appl
9	17	US-10-888-348-157	Sequence 157, Appl
10	14	US-10-146-130-39	Sequence 39, Appl
10	16	US-10-657-022-387	Sequence 387, Appl
10	16	US-10-657-022-389	Sequence 389, Appl
10	16	US-10-657-022-392	Sequence 392, Appl
10	16	US-10-657-022-394	Sequence 394, Appl
12	14	US-10-146-130-36	Sequence 36, Appl
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14	14	US-10-146-130-37	Sequence 37, Appl
14	14	US-10-153-334-17	Sequence 17, Appl
15	14	US-10-146-130-38	Sequence 38, Appl
15	14	US-10-161-499-66	Sequence 66, Appl
15	17	US-10-744-964-66	Sequence 66, Appl
16	14	US-10-146-130-33	Sequence 33, Appl
16	14	US-10-153-334-13	Sequence 13, Appl
17	14	US-10-153-334-16	Sequence 16, Appl
18	14	US-10-146-130-12	Sequence 12, Appl
30	15	US-10-296-734-1384	Sequence 1384, Ap
30	15	US-10-296-734-1386	Sequence 1386, Ap
31	15	US-10-394-511-108	Sequence 108, Appl
31	16	US-10-651-584C-58	Sequence 58, Appl
32	9	US-09-864-761-37322	Sequence 37322, A
33	14	US-10-195-730-367	Sequence 367, Appl
33	16	US-10-799-747-367	Sequence 367, Appl
33	17	US-10-979-183-367	Sequence 367, Appl
36	15	US-10-424-599-159544	Sequence 159544,
36	15	US-10-424-599-248110	Sequence 248110,
38	15	US-10-424-599-178775	Sequence 178775,
38	16	US-10-425-115-189470	Sequence 189470,
38	16	US-10-425-115-286847	Sequence 286847,
39	16	US-10-425-115-299407	Sequence 299407,
39	17	US-10-900-680-4	Sequence 4, Appl1
40	10	US-09-764-891-3493	Sequence 3493, Ap
41	16	US-10-437-963-201259	Sequence 201259,
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42	16	US-10-425-115-364790	Sequence 364790,
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45	15	US-10-424-599-161949	Sequence 161949,
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46	16	US-10-425-115-315130	Sequence 315130,
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48	16	US-10-437-963-172496	Sequence 172496,
49	15	US-10-424-599-224012	Sequence 224012,
49	16	US-10-425-115-349760	Sequence 349760,
50	11	US-09-864-408A-8876	Sequence 8876, Ap
50	11	US-09-855-604-775	Sequence 775, Appl
50	16	US-10-425-115-258682	Sequence 258682,
51	9	US-09-796-692-1075	Sequence 1075, Ap

85 21 100.0 51 14 US-10-040-862-1075 Sequence 1075, Ap
86 21 100.0 51 15 US-10-057-475B-1075 Sequence 1075, Ap
87 21 100.0 51 15 US-10-154-884B-1075 Sequence 1075, Ap
88 21 100.0 51 15 US-10-424-599-270511 Sequence 270511, Ap
89 21 100.0 51 16 US-10-764-324-1075 Sequence 1075, Ap
90 21 100.0 52 10 US-09-764-891-5266 Sequence 5266, Ap
91 21 100.0 52 15 US-10-424-599-249890 Sequence 249890, Ap
92 21 100.0 52 16 US-10-425-115-251053 Sequence 251053, Ap
93 21 100.0 53 9 US-09-982-610-6 Sequence 6, Appli
94 21 100.0 54 15 US-10-424-599-158105 Sequence 158105, Ap
95 21 100.0 54 16 US-10-437-963-125127 Sequence 125127, Ap
96 21 100.0 55 15 US-10-424-599-242044 Sequence 242044, Ap
97 21 100.0 55 16 US-10-425-115-269005 Sequence 269005, Ap
98 21 100.0 55 17 US-10-741-600-1528 Sequence 1528, Ap
99 21 100.0 55 17 US-10-741-600-1532 Sequence 1532, Ap
100 21 100.0 56 15 US-10-424-599-221947 Sequence 221947, Ap

ALIGNMENTS

RESULT 1

US-10-146-130-16

; Sequence 16, Application US/10146130

; Publication No. US20030004107A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF

; FILE OF INVENTION: NEURAL THREAD PROTEINS

; FILE REFERENCE: 59003.000007

; CURRENT APPLICATION NUMBER: US/10/146.130

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-146-130-16

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 1 HARL 4

RESULT 2

US-10-146-130-15

; Sequence 15, Application US/10146130

; Publication No. US20030004107A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF

; FILE OF INVENTION: NEURAL THREAD PROTEINS

; FILE REFERENCE: 59003.000007

; CURRENT APPLICATION NUMBER: US/10/146.130

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-146-130-15

Query Match 100.0%; Score 21; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 2 HARL 5
RESULT 3
US-10-146-130-17
; Sequence 17, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-17

Query Match 100.0%; Score 21; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 1 HARL 4

RESULT 4

US-10-146-130-18

; Sequence 18, Application US/10146130

; Publication No. US20030004107A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF

; FILE OF INVENTION: NEURAL THREAD PROTEINS

; FILE REFERENCE: 59003.000007

; CURRENT APPLICATION NUMBER: US/10/146.130

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-146-130-18

Query Match 100.0%; Score 21; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Db 1 HARL 4

RESULT 5

US-10-146-130-24

; Sequence 24, Application US/10146130

; Publication No. US20030004107A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF

; FILE OF INVENTION: NEURAL THREAD PROTEINS

; FILE REFERENCE: 59003.000007

; CURRENT APPLICATION NUMBER: US/10/146.130

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-24

Query Match 100.0%; Score 21; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 1 HARL 4

RESULT 6

US-10-146-130-31
; Sequence 31, Application US/10146130
; Publication No. US20030004107A1

; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-31

Query Match 100.0%; Score 21; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 1 HARL 4

RESULT 7

US-10-146-130-41
; Sequence 41, Application US/10146130
; Publication No. US20030004107A1

; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-41

Query Match 100.0%; Score 21; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 1 HARL 4

RESULT 8

US-10-146-130-42

; Sequence 42, Application US/10146130
; Publication No. US20030004107A1

; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-42

Query Match 100.0%; Score 21; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 1 HARL 4

RESULT 9

US-10-146-130-19
; Sequence 19, Application US/10146130
; Publication No. US20030004107A1

; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-19

Query Match 100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 2 HARL 5

RESULT 10

US-10-146-130-21
; Sequence 21, Application US/10146130
; Publication No. US20030004107A1

; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-21

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Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 11
US-10-146-130-22
; Sequence 22, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-22

Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 12
US-10-935-254-10
; Sequence 10, Application US/10935254
; Publication No. US20050054752A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Jianjun P
; TITLE OF INVENTION: Peptide-Based Diblock and Triblock Dispersants
; FILE REFERENCE: C62252 US NA
; CURRENT APPLICATION NUMBER: US/10/935.254
; CURRENT FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pigment Binding Peptide
US-10-935-254-10

Query Match      100.0%; Score 21; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 13
US-10-146-130-40
; Sequence 40, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
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```
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-40

Query Match      100.0%; Score 21; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 14
US-10-657-022-390
; Sequence 390, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657.022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-390

Query Match      100.0%; Score 21; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 15
US-10-657-022-396
; Sequence 396, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657.022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 8
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; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-396

Query Match 100.0%; Score 21; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 1 HARL 4

RESULT 16

US-10-931-627-15
; Sequence 15, Application US/10931627
; Publication No. US20050106100A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb
; APPLICANT: Harris, Thomas D.
; APPLICANT: Yamamanchili, Padmaja
; TITLE OF INVENTION: COMPOUNDS CONTAINING MATRIX METALLOPROTEINASE SUBSTRATES AND
; TITLE OF INVENTION: METHODS OF THEIR USE
; FILE REFERENCE: PH7492 NP
; CURRENT APPLICATION NUMBER: US/10/931,627
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 60/499,960
; PRIOR FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/499,966
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Polypeptide
US-10-931-627-15

Query Match 100.0%; Score 21; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 17

US-10-657-022-388
; Sequence 388, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-388

Query Match 100.0%; Score 21; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 6 HARL 9

RESULT 18

US-10-657-022-391
; Sequence 391, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-391

Query Match 100.0%; Score 21; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 19

US-10-657-022-393
; Sequence 393, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-393

Query Match 100.0%; Score 21; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 20

US-10-657-022-395
; Sequence 395, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPIOTOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 395
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-395

Query Match 100.0%; Score 21; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 21
US-10-657-022-397
; Sequence 397, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPIOTOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-397

Query Match 100.0%; Score 21; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 1 HARL 4

RESULT 22
US-10-888-348-32
; Sequence 32, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348

; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-32

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 23
US-10-888-348-36
; Sequence 36, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-36

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 24
US-10-888-348-37
; Sequence 37, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08

; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-37

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 25

US-10-888-348-41
; Sequence 41, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-41

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 26

US-10-888-348-69
; Sequence 69, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-69

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 27

US-10-888-348-77
; Sequence 77, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-77

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 28

US-10-888-348-84
; Sequence 84, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; TITLE OF INVENTION: CILIARY NEUTROTROPIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-84

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 29
US-10-888-348-88
; Sequence 88, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPHIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-88

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 30
US-10-888-348-102
; Sequence 102, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPHIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-102

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 HARL 8

RESULT 31
US-10-888-348-153
; Sequence 153, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPHIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 153
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-153

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 32
US-10-888-348-154
; Sequence 154, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUTROTROPHIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-888-348-154

Query Match 100.0%; Score 21; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 33

US-10-657-022-392

Query Match 100.0%; Score 21; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 4 HARL 7

RESULT 38

US-10-657-022-394
; Sequence 394, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 394
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homosapiens

US-10-657-022-394

Query Match 100.0%; Score 21; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 39

US-10-146-130-36
; Sequence 36, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-146-130-36

Query Match 100.0%; Score 21; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 40

US-10-146-130-35

; Sequence 35, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-146-130-35

Query Match 100.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 9 HARL 12

RESULT 41

US-10-146-130-37
; Sequence 37, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-146-130-37

Query Match 100.0%; Score 21; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 5 HARL 8

RESULT 42

US-10-153-334-17
; Sequence 17, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: PRT

US-10-146-130-35

```
; ORGANISM: Homo sapiens
US-10-153-334-17

Query Match      100.0%; Score 21; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 4 HARL 7

RESULT 43
US-10-146-130-38
; Sequence 38, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-38

Query Match      100.0%; Score 21; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 11 HARL 14

RESULT 44
US-10-161-499-66
; Sequence 66, Application US/10161499
; Publication No. US2003004427A1
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M36A
US-10-161-499-66

Query Match      100.0%; Score 21; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 45
US-10-744-964-66
; Sequence 66, Application US/10744964
; Publication No. US20050085411A1
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/744,964
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M36A
US-10-744-964-66

Query Match      100.0%; Score 21; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 46
US-10-146-130-33
; Sequence 33, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-33

Query Match      100.0%; Score 21; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 47
US-10-153-334-13
; Sequence 13, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
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; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-13

Query Match      100.0%; Score 21; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      4 HARL 7

RESULT 48
US-10-153-334-46
; Sequence 46, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-46

Query Match      100.0%; Score 21; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      5 HARL 8

RESULT 49
US-10-146-130-12
; Sequence 12, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003-000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-12

Query Match      100.0%; Score 21; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      1 HARL 4

RESULT 50
US-10-296-734-1384
; Sequence 1384, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1384
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PRAME segment 31
US-10-296-734-1384

Query Match      100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      16 HARL 19

RESULT 51
US-10-296-734-1386
; Sequence 1386, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1386
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PRAME segment 32
US-10-296-734-1386

Query Match      100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HARL 4
Db      1 HARL 4

RESULT 52
US-10-394-511-108
```

```
; Sequence 108, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant preproinsulin linker region for MMP-11, PAP-284
; US-10-394-511-108

Query Match      100.0%; Score 21; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HARL 4
DB      20 HARL 23

RESULT 53
US-10-651-584C-58
; Sequence 58, Application US/10651584C
; Publication No. US20040259768A1
; GENERAL INFORMATION:
; APPLICANT: Lauermann, Vit
; TITLE OF INVENTION: Targeted release
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/651,584C
; CURRENT FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 58
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mammalian, peptide specifically cleavable by a reagent produced b
; US-10-651-584C-58

Query Match      100.0%; Score 21; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HARL 4
DB      20 HARL 23

RESULT 54
US-09-864-761-37322
; Sequence 37322, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

```
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37322
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049633.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.3
; US-09-864-761-37322

Query Match      100.0%; Score 21; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HARL 4
DB      12 HARL 15

RESULT 55
US-10-195-730-367
; Sequence 367, Application US/10195730
; Publication No. US20030144492A1
```

; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 367
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-730-367

Query Match 100.0%; Score 21; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 12 HARL 15

RESULT 56
US-10-799-747-367
; Sequence 367, Application US/10799747
; Publication No. US20040157258A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/799,747
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/10/195,730
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 367
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-799-747-367

Query Match 100.0%; Score 21; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 12 HARL 15

RESULT 57
US-10-979-183-367
; Sequence 367, Application US/10979183
; Publication No. US20050069943A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/979,183

; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/10/799,747
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/10/195,730
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 367
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-183-367

Query Match 100.0%; Score 21; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 12 HARL 15

RESULT 58
US-10-424-599-159544
; Sequence 159544, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159544
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115088C.1.pap
US-10-424-599-159544

Query Match 100.0%; Score 21; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 13 HARL 16

RESULT 59
US-10-424-599-248110
; Sequence 248110, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248110
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66073C.1.pep
US-10-424-599-248110

Query Match 100.0%; Score 21; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 25 HARL 28

RESULT 60

US-10-424-599-178775
; Sequence 178775, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 178775
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132450C.1.pep
US-10-424-599-178775

Query Match 100.0%; Score 21; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 21 HARL 24

RESULT 61

US-10-425-115-189470
; Sequence 189470, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 189470
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_104381C.1.pep
US-10-425-115-189470

Qy 1 HARL 4
Db 22 HARL 25

Query Match 100.0%; Score 21; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 24 HARL 27

RESULT 62

US-10-425-115-286847
; Sequence 286847, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286847
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_2469C.1.pep
US-10-425-115-286847

Query Match 100.0%; Score 21; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 20 HARL 23

RESULT 63

US-10-425-115-299407
; Sequence 299407, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 299407
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_36129C.1.pep
US-10-425-115-299407

Query Match 100.0%; Score 21; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 22 HARL 25

RESULT 64

US-10-900-680-4
; Sequence 4, Application US/10900680
; Publication No. US20050037432A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Arner, Elizabeth
; APPLICANT: Tortorella, Micky
; APPLICANT: Malfait, Anne-Marie
; TITLE OF INVENTION: Novel Biomarkers of Aggreanase Activity
; FILE REFERENCE: 01194
; CURRENT APPLICATION NUMBER: US/10/900,680
; CURRENT FILING DATE: 2004-07-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-900-680-4

Query Match 100.0%; Score 21; DB 17; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 28 HARL 31

RESULT 65

US-09-764-891-3493
; Sequence 3493, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3493
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3493

Query Match 100.0%; Score 21; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 32 HARL 35

RESULT 66

US-10-437-963-201259
; Sequence 201259, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201259
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96652C.1.pep
US-10-437-963-201259

Query Match 100.0%; Score 21; DB 16; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 3 HARL 6

RESULT 67

US-10-425-115-237297
; Sequence 237297, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237297
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(41)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_1479C.1.pep
US-10-425-115-237297

Query Match 100.0%; Score 21; DB 16; Length 41;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 68

US-10-424-599-177046
; Sequence 177046, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177046
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(42)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130890C.1.pep
US-10-424-599-177046

Query Match 100.0%; Score 21; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 8 HARL 11

RESULT 69
US-10-425-115-364790
; Sequence 364790, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 364790
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_95856C.1.pep
US-10-425-115-364790

Query Match 100.0%; Score 21; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 17 HARL 20

RESULT 70
US-10-424-599-202467
; Sequence 202467, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 202467
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24853C.1.pep
US-10-424-599-202467

Query Match 100.0%; Score 21; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 15 HARL 18

RESULT 71
US-10-424-599-161949
; Sequence 161949, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161949
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117258C.1.pep
US-10-424-599-161949

Query Match 100.0%; Score 21; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 28 HARL 31

RESULT 72
US-10-424-599-274063
; Sequence 274063, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274063
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8949C.1.pep
US-10-424-599-274063

Query Match 100.0%; Score 21; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 17 HARL 20

RESULT 73

US-10-425-115-315130
; Sequence 315130, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315130
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_50458C.1.pep
US-10-425-115-315130

Query Match 100.0%; Score 21; DB 16; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 5 HARL 8

RESULT 74

US-10-424-599-170899
; Sequence 170899, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170899
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125336C.1.pep
US-10-424-599-170899

Query Match 100.0%; Score 21; DB 15; Length 47;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
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Db 38 HARL 41

RESULT 75

US-10-425-115-267080
; Sequence 267080, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267080
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175177C.1.pep
US-10-425-115-267080

Query Match 100.0%; Score 21; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
|||
Db 38 HARL 41

Search completed: July 5, 2005, 16:39:04
Job time : 161 secs